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OM protein - protein search, using sw mode.i

Run on: April 24, 2003, 10:17:37 ; Search time 25 Seconds

Minimum DB seq length: 0 (without alignments)
Maximum DB seq length: 2000000000 (Rel. 40, last sequence update)

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	226	1 KAD3_HUMAN	Q9UJ7 hom sapien
2	84	95.5	226	1 KAD3_BOVIN	P08760 bos taurus
3	84	95.5	226	1 KAD3_RAT	P29411 rattus norv
4	77	87.5	223	1 KAD4_HUMAN	P27144 homo sapien
5	77	87.5	223	1 KAD4_MOUSE	Q9W9Q9 mus musculus
6	77	87.5	223	1 KAD4_RAT	Q9W9Q9 rattus norv
7	75	85.5	219	1 KAD3_MOUSE	Q9W9P7 mus musculus
8	70.5	214	1 KAD_MCGA	Q52522 mycoplasma	
9	62	225	1 KAD2_YEAST	P26564 saccharomyces	
10	61	69.3	245	1 KAD_CHLTR	Q84130 chlamydia t
11	61	69.3	253	1 KAD_CHLMLU	Q9PKR0 chlamydia m
12	60	68.2	215	1 KAD_PSEAU	Q9H9V4 pseudomonas
13	60	68.2	216	1 KAD_PSEPU	Q9ZQ09 pseudomonas
14	60	68.2	231	1 KAD2_MOUSE	Q9W9P6 mus musculus
15	60	68.2	238	1 KAD2_HUMAN	P54119 homo sapien
16	60	68.2	251	1 KAD2_RAT	P29410 rattus norv
17	60	68.2	251	1 KAD_CAEEL	P34446 caenorhabdi
18	59	67.0	214	1 KAD_ECOLI	P05982 escherichia
19	59	67.0	214	1 KAD_SALTY	P37407 salmonella
20	59	67.0	214	1 KAD_VIBCH	Q9K1B7 vibrio chol
21	59	67.0	214	1 KAD_YEREN	P43112 yersinia en
22	59	67.0	214	1 KAD_YERPE	Q69172 yersinia pe
23	59	67.0	215	1 KAD_BUCAI	P57556 buchnera ap
24	59	67.0	215	1 KAD_NEIGO	P49979 neisseria g
25	59	67.0	215	1 KAD_NEIMA	P49980 neisseria m
26	59	67.0	222	1 KAD_RALSO	Q8XW61 ralstonia s
27	59	67.0	240	1 KAD2_BOVIN	P08166 bos taurus
28	59	67.0	248	1 KAD_GIRALA	P49982 giardia lam
29	58	65.9	187	1 KAD_XYLFA	Q9PBM3 xylolla fas
30	58	65.9	443	1 ERAL_HUMAN	Q75516 homo sapien
31	57	64.8	205	1 KAD_MICLU	P33107 micrococcus
32	56	63.6	181	1 KAD_MICLE	Q33007 mycobacteri
33	56	63.6	213	1 KAD_CHLPN	Q9zB00 chlamydia p

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ALIGNMENTS

RESULT 1

KAD3_HUMAN STANDARD: PRT: 226 AA.

ID: Q9UJ7; AC: DT: 16-OCT-2001 (Rel. 40, Created)

DT: 16-OCT-2001 (Rel. 40, Last sequence update)

DT: 16-OCT-2001 (Rel. 40, Last annotation update)

DE: GTP:AMP phosphotransferase mitochondrial (EC 2.7.4.10) (AK3), (AK3- alpha).

DE: AK3.

GN: KAD3_HUMAN

OS: Homo sapiens (Human).

OC: Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX: NCBI-TAXID=9606;

RN: [1]

RP: SEQUENCE FROM N.A.

RC: TISSUE=Liver;

RA: Noma T.;

RL: Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.

CC: - - - CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.

CC: - - - SUBUNIT: MONOMER (By SIMILARITY).

CC: - - - SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).

CC: - - - SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.

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CC: DR: EMBL: AB021870; BAA87913.1; -.

DR: HSSP: P08760; 2AK3.

DR: InterPro: IPR000850; Adenylate_kinase.

DR: Pfam: PF00406; adenylate_kinase_1.

PRINS: PR00054; ADENYLYLKINASE.

DR: PRODOM: PD00057; Adenylylate_kin_1.

DR: PROSITE: PS00113; ADENYLYLATE_KINASE_1.

KW: Transferase; Kinase; GTP-binding; Mitochondrion.

FT: INT_MET: 0 BY SIMILARITY.

FT: NP-BIND: 0

FT: SEQUENCE: 226 AA: 25507 MW: 9E+23E32A96B0C3 CRC64: 1 RLLRAVIMAPGSGKTV 18

Query Match: 100.0%; Score: 88; DB: 1; Length: 226; Best Local Similarity: 100.0%; Pred. No.: 9.9e-06; Matches: 18; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

Db: 5 RLLRAVIMAPGSGKTV 22

AC P08760;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.7.4.10) (AK3).
 GN AK3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID:9913;
 RN [1] SEQUENCE FROM N.A. PubMed=2478555;
 RX MEDLINE=90037053;
 RA Yamada M., Shahjahan M., Tanabe T., Kishi F., Nakazawa A.;
 RT "Cloning and characterization of cDNA for mitochondrial GTP:AMP
 phosphotransferase of bovine liver."
 RL J. Biol. Chem. 264:19192-19199(1989).
 RN [2] SEQUENCE.
 RP TISSUE=Heart;
 RX MEDLINE=86248102; PubMed=3013690;
 RA Tomasselli A.G., Frank R., Schultz E.;
 RT "the complete primary structure of GTP:AMP phosphotransferase from
 beef heart mitochondria."
 RL FEBS Lett. 202:303-308(1986).
 RN [3] SEQUENCE OF 1-49 FROM N.A.
 RX MEDLINE=92054124; PubMed=1148300;
 RA Shahjahan M., Yamada M., Tanaka H., Nakazawa A.;
 RT "Cloning and characterization of the gene encoding bovine
 mitochondrial adenylyl kinase isozyme 3."
 RL Gene 107:313-317(1991).
 RN [4] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=91084487; PubMed=2175649;
 RA Diederichs K., Schulz G.E.;
 RT "Three dimensional structure of the complex between adenylyl kinase from
 matrix adenylyl kinase and its substrate AMP."
 RN [5] X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
 RX MEDLINE=91132661; PubMed=1994037;
 RA Diederichs K., Schulz G.E.;
 RT "The refined structure of the complex between adenylyl kinase from
 beef heart mitochondrial matrix and its substrate AMP at 1.85-A
 resolution."
 RL J. Mol. Biol. 217:541-549(1991).
 CC -1 - CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.
 CC -1 - SUBUNIT: MONOMER.
 CC -1 - SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1 - SIMILARITY: BELONGS TO THE ADENYLYL KINASE FAMILY.
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 CC -----
 DR PRODOM: PD000657; Adenylyl_kin; 1.
 DR PROSITE: PS00113; ADENYLYL_KINASE; 1.
 KW Transferase; Kinase; GTP-binding; Mitochondrion; 3D-structure.
 FT INIT_MET 0 0 GTP (BY SIMILARITY).
 FT NP_BIND 13 21 GTP (BY SIMILARITY).
 FT CONFLICT 10 21 MISSING (IN REF. 2).
 FT STRAND 8 12
 FT TURN 15 16
 FT HELIX 19 29
 FT STRAND 33 36
 FT STRAND 86 89
 FT HELIX 37 45
 FT HELIX 95 102
 FT TURN 46 48
 FT HELIX 50 60
 FT TURN 61 62
 FT HELIX 67 79
 FT TURN 80 81
 FT HELIX 86 89
 FT STRAND 127 130
 FT STRAND 125 125
 FT TURN 127 130
 FT STRAND 131 134
 FT TURN 135 138
 FT STRAND 139 141
 FT TURN 142 142
 FT STRAND 147 148
 FT TURN 149 149
 FT STRAND 151 153
 FT TURN 156 156
 FT STRAND 158 158
 FT TURN 161 162
 FT HELIX 165 189
 FT TURN 190 190
 FT STRAND 192 196
 FT HELIX 200 212
 FT TURN 213 214
 FT SEQUENCE 226 AA; 2554 MW; 2B74C2FBAAA7CBA9 CRC64;
 DR Query Match 95.5%; Score 84; DB 1; Length 226;
 DR Best Local Similarity 94.4%; Pred. No. 3.5e-05;
 DR Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DR RESULT 3
 DR KAD3_RAT STANDARD; PRT; 226 AA.
 DR ID P29411;
 DR DT 01-APR-1993 (Rel. 25, Created)
 DR DT 01-APR-1993 (Rel. 25, Last sequence update)
 DR DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DR DE GTP:AMP phosphotransferase mitochondrial (EC 2.7.7.4.10) (AK3).
 DR GN AK3.
 DR OS Rattus norvegicus (Rat).
 DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 DR OX NCBI_TaxID:10116;
 DR RN [1] SEQUENCE FROM N.A.
 DR RX MEDLINE=9322400; PubMed=8468325;
 DR RA Tanabe T., Yamada M., Noma T., Kajii T., Nakazawa A.;
 DR RT "Tissue-specific and developmentally regulated expression of the
 genes encoding adenylyl kinase isozymes."
 DR RL J. Biochem. 113:200-207(1993).
 DR CC -1 - CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.
 DR CC -1 - SUBUNIT: MONOMER.
 DR CC -1 - SUBCELLULAR LOCATION: Mitochondrial matrix.
 DR -1 - SIMILARITY: BELONGS TO THE ADENYLYL KINASE FAMILY.

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DR PIR; D13062; BAA2379.1;
 DR PIR; J01945; J01945.
 DR InterPro; IPR000850; Adenylate_kin.
 DR Pfam; PF00405; adenylatekinase; 1.
 DR PRINTS; PR00054; ADENYLTKNASE.
 DR PRODOM; PD00657; Adenylate_kin; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 DR TRANSFERASE; Kinase; GTP-binding; Mitochondrion.
 DR INIT_MET 0 BY SIMILARITY.
 DR NP_BIND 13 21 GTP (BY SIMILARITY).
 DR SEQUENCE 226 AA; 25307 MW; D57FF37404AA6625 CRC64;

Query Match 95.5%; Score 84; DB 1; Length 226;
 Best Local Similarity 100%; Pred. No. 3.5e-05; Mismatches 0; Indels 0; Gaps 0;
 Matches 17; Conservative 17

Qy 1 RLLRAVIMGAPGSGKGT 17
 Db 5 RLLRAVIMGAPGSGKGT 21

RESULT 4

KAD4_HUMAN	STANDARD;	PRT;	223 AA.
AC P27744;			
DT 01-AUG-1992 (Rel. 23, Created)			
DT 01-AUG-1992 (Rel. 23, Last sequence update)			
DT 15-JUN-2002 (Rel. 41, Last annotation update)			
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP			
GN AK4			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=92347846; PubMed=1639383;			
RT "Characterization of human adenylate kinase 3 (AK3) cDNA and mapping			
RT of the AK3 pseudogene to an intron of the NFL gene.",			
RT Genomics 13:537-542(1992).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=92347846; PubMed=1639383;			
RA Xu G., O'Connell P., Stevens J., White R.;			
RT "Identification of a novel adenylate kinase system in the brain: cloning of the fourth adenylate kinase.",			
RT Brain Res. Mol. Brain Res. 62:187-195(1998).			
RN [2]			
RP SEQUENCE FROM N.A.			
RX MEDLINE=92347846; PubMed=1639383;			
RA Strausberg R.;			
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.			
CC			
CC -!- CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.			
CC -!- SUBUNIT: MONOMER.			
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential).			
CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.			
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DR EMBL; X60673; CAA4088.1; -.			
DR EMBL; BC016180; AAH16180.1; -.			
DR PIR; S16381; S16381.			

DR PIR; S16380; S16380.
 DR PIR; A42820; A42820.
 DR HSSP; P08760; 2AK3.
 DR Genew; HGNC; 363; AK3.
 DR MIM; 103030; -.
 DR InterPro; IPR000850; Adenylate_kin.
 DR Pfam; PF00406; adenylatekinase; 1.
 DR PRINTS; PR00094; ADENYLTKNASE.
 DR PRODOM; PD00657; Adenylate_kin; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 DR TRANSFERASE; Kinase; GTP-binding; Mitochondrion.
 DR NP_BIND 12 20 GTP (BY SIMILARITY).
 DR SEQUENCE 223 AA; 25268 MW; 653341A8EB3BC/23 CRC64;
 DR PIR; S16381; S16381.

Query Match 87.5%; Score 77; DB 1; Length 223;
 Best Local Similarity 83.3%; Pred. No. 0.0035; Mismatches 2; Indels 0; Gaps 0;
 Matches 15; Conservative 15; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 RLLRAVIMGAPGSGKGT 18
 Db 4 KLLRAVILGPAGSGKGT 21

RESULT 5

KAD4_MOUSE	STANDARD;	PRT;	223 AA.
AC Q9WUR9; Q9R1X7;			
DT 30-MAY-2000 (Rel. 39, Created)			
DT 30-MAY-2000 (Rel. 39, Last sequence update)			
DT 16-OCT-2001 (Rel. 40, Last annotation update)			
DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP			
DE transphosphorylase).			
DR NCBITaxID=10090;			
DR NCBI_TaxID=10090;			
DR MUS musculus (Mouse).			
DR Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.			
DR Yoneda T., Saito M., Maeda M., Takagi H.;			
RT MEDLINE=99033072; PubMed=9813319;			
RT TISSUE=Brain;			
RT "Identification of a novel adenylate kinase system in the brain: cloning of the fourth adenylate kinase.",			
RT Brain Res. Mol. Brain Res. 62:187-195(1998).			
RN [2]			
RP SEQUENCE FROM N.A.			
RA Noma T.;			
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.			
CC -!- CATALYTIC ACTIVITY: GTP + AMP = GDP + ADP.			
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential).			
CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE PYRAMIDAL CELLS IN THE			
CC HIPPOCAMPUS.			
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A			
CC REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO			
CC THE ADULTHOOD IN THE RODENT.			
CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.			
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DR EMBL; D85036; BAA7760.1; -.			
DR EMBL; AB02039; BAA77363.1; -.			
DR HSSP; P08760; 2AK3.			
DR MGII; MGII; 87980; Ak4.			
DR InterPro; IPR000850; Adenylate_kin.			
DR Pfam; PF00406; adenylatekinase; 1.			
DR PRINTS; PR00094; ADENYLTKNASE.			

DR PRODOM: PD000657; Adenylate_kin; 1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
 KW Transferase; GTP-binding; Mitochondrion.
 FT NP_BIND: 12 20 GTP (BY SIMILARITY).
 FT CONFLICT 68 68 V -> A (IN REF. 2);
 FT CONFLICT 187 187 S -> N (IN REF. 2);
 FT CONFLICT 190 190 V -> M (IN REF. 2);
 SQ SEQUENCE 223 AA; 25061 MW; 50552294971515EC CRC64;
 QY 1 RLIRAVIMGAPGSQGKTV 18
 :|||||||:|||||||
 Db 4 KLLRAVILGPPGSGKGTV 21

RESULT 6
 KADA_RAT STANDARD: PRT; 223 AA.
 ID KADA_RAT STANDARD: PRT; 223 AA.
 AC Q9WNU0; 1.
 DT 30-MAY-2000 (Rel. 39, created)
 DT 30-MAY-2000 (Rel. 39, last sequence update)
 DE Adenylate kinase isoenzyme 4, mitochondrial (EC 2.7.4.3) (ATP-AMP
 DE transphosphorylase).
 AK4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 OC NCBI_TaxID=10090;
 RN [1]
 RP STRAIN=Iwistar; TISSUE=forebrain;
 RX MEDLINE=9903072; PubMed=9833319;
 RA Yoneda T., Sato M., Maeda M., Takagi H.;
 RT "Identification of a novel adenylyl kinase system in the brain:
 cloning of the fourth adenylyl kinase.";
 RL Brain Res. Mol. Brain Res. 65:187-195(1998).
 CC -!- CATALYTIC ACTIVITY: GTP + AMP = GTP + ADP.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix (Potential).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE PYRAMIDAL CELLS IN THE
 CC HIPPOCAMPUS.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE CENTRAL NERVOUS SYSTEM IN A
 CC REGION-SPECIFIC MANNER FROM THE MIDDLE STAGE OF EMBRYOGENESIS TO
 CC THE ADULTHOOD IN THE RODENT.
 CC -!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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 DR EMBL; AB020203; BAA77360.1; -.
 DR HSSP; P03760; 2AK3.
 DR MGII; 87979; AK3.
 DR InterPro; IPR000850; Adenylate_kin.
 DR Pfam; PF00406; adenylatekinase; 1.
 DR PRINTS; PR00094; ADENYLTKNASE.
 DR PRODOM; PD000657; ADENYLATE_KINASE; 1.
 DR PROSITE: PS00113; ADENYLATE_KINASE; 1.
 KW Transferase; Kinase; GTP-binding; Mitochondrion.
 FT NP_BIND: 6 14 GTP (BY SIMILARITY).
 SQ SEQUENCE 219 AA; 24640 MW; 7DBB8DFA2C0BEB7C5 CRC64;
 QY 4 RAVIMGAPGSQGKTV 18
 :|||||||
 DB 1 RAVIMGAPGSQGKTV 15

Query Match 85.2%; Score 75; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 0.00066; Mismatches 0; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 8
 KAD_MYCGA STANDARD: PRT; 214 AA.
 ID KAD_MYCGA STANDARD: PRT; 214 AA.
 AC Q9WNU7; 1.
 DT 30-MAY-2000 (Rel. 39, created)
 DT 30-MAY-2000 (Rel. 39, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 GN ADK
 OS Mycoplasma gallidisepticum
 OS Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A5969var.B.
 RA Skamrov A., Feoktistova E., Goldman M., Beabalaashvili R.,

QY 1 RLIRAVIMGAPGSQGKTV 18

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CC EMBL; AE001286; AAC67719.1; -.

CC HSSP; P08760; 2AK3.

CC InterPro; IPR000850; Adenylate_kin.

CC Pfam; PF00406; adenylatekinase; 1.

CC PRINS; PR00094; ADENYLTKNASE.

CC PRODOM; PD000857; Adenylate_kin; 1.

DR PROBOM; PD00057; Adenylate_kin; 1.

DR PROSITE; PS00113; ADENYLATE_KINASE; 1.

DR KW Transferase; Kinase; ATP-binding; Complete proteome.

DR FT NP_BIND; 12; 20 ATP (BY SIMILARITY).

DR SEQUENCE 253 AA; 28597 MW; 9F915F6EFCB6AF0D CRC64;

CC Query Match 69 3%; Score 61; DB 1; Length 245;

CC Best Local Similarity 91 7%; Pred. No. 0.076; 0; Indels 0; Gaps 0;

CC Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CC Qy 6 VIMGAPGSGKGT 17

Db 9 IIMGAPGSGKGT 20

RESULT 11

ID	KAD_CHLMU	STANDARD:	PRT:	253 AA.
AC	Q9PRR0;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DE	Adenylyl kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).			
GN	ADK OR TCO0404.			
OS	Chlamydia muridarum.			
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.			
OX	NCBI_TAXID=83560;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=AVCC 15692 / PAO1;			
RX	MEDLINE=20437337; PubMed=10984043;			
RA	Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,			
RA	Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,			
RA	Gardner R.L., Coltrin L., Tolentino E., Westbroek-Wadman S., Yuan Y.,			
RA	Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,			
RA	Smith K.A., Spener D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,			
RA	Reiser J., Sauer M.H., Hancock R.E.W., Lory S., Olson M.V.,			
RA	"Complete genome sequence of <i>Pseudomonas aeruginosa</i> PAO1, an opportunistic pathogen,"			
RL	Nature 406:959-964(2000).			
CC	-!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR			
CC	MAINTENANCE AND CELL GROWTH.			
CC	-!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.			
CC	-!- SUBUNIT: MONOMER (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).			
CC	-!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AE002307; AAC39261.1; -.			
CC	DR EMBL; AE004788; AAC07074.1; -.			
CC	DR HSSP; P05082; 1E4V.			
CC	DR InterPro; IPR000850; Adenylate_kin.			
CC	DR Pfam; PF00406; adenylatekinase; 1.			
CC	DR PRINS; PR00094; ADENYLTKNASE.			
CC	DR PROBOM; PD00057; Adenylate_kin; 1.			
CC	DR PROSITE; PS00113; ADENYLATE_KINASE; 1.			
CC	DR KW Transferase; Kinase; ATP-binding; Complete proteome.			
CC	DR NP_BIND; 7; 15 ATP (BY SIMILARITY).			
CC	DR SEQUENCE 215 AA; 23107 MW; 744C9F0C51E1C007 CRC64;			
CC	Query Match 68 2%; Score 60; DB 1; Length 215;			
CC	Best Local Similarity 60 0%; Pred. No. 0.09; 0; Indels 0; Gaps 0;			
CC	Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;			
CC	Qy 3 LRAVIMGAPGSGKGT 17			
Db 1 MRVILLGAGAGKGT 15				

RL Submitted (Nov-1998) to the EMBL/GenBank/NCBI databases.
 CC -!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
 CC -!- CATALYTIC ACTIVITY: ATP + AMP ADP + ADP.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial intermembrane space (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AB020202; BAA77359.1; -
 DR HSSP; P08166; IAK2.
 DR MGDB; MG1:8798; AK2.
 DR Submitted (MAR-1999) to the EMBL/GenBank/NCBI databases.
 DR -!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC MAINTENANCE AND CELL GROWTH.
 CC -!- CATALYTIC ACTIVITY: ATP + AMP ADP + ADP.
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
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 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 DR EMBL; AB024426; BAA75010.1; -
 DR HSSP; P05082; IAK2.
 DR InterPro; IPR00050; Adenylyl kinase.
 DR Pfam; PF0006; adenylyl kinase_1.
 DR PRINTS; PRO0094; ADENYLTKNASE.
 DR PRODOM; PD000657; Adenylyl kinase_1.
 DR PROSITE; PS00113; ADENYLYL_KINASE_1.
 DR Transferase; Kinase; ATP-binding.
 DR KW Transferase; Kinase; ATP-binding; Mitochondrion.
 DR FT INT_MET 21 29 ATP (BY SIMILARITY).
 DR NP_BIND 0 BY SIMILARITY.
 DR SEQUENCE 231 AA; 25693 MW; A90DA6797CPB6E1E CRC64;
 DR
 DR Query Match 68.2%; Score 60; DB 1; Length 231;
 DR Best Local Similarity 66.7%; Pred. No. 0.097;
 DR Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 DR
 DR QY 3 LRAVIMGAPGSGKGT 17
 DR Db 15 ITRAVLGLGPAGKGT 29
 DR
 DR RESULT 15
 DR KAD2_HUMAN
 DR KAD2_HUMAN STANDARD; PRT; 238 AA.
 DR AC P58191; Q16836;
 DR DT 01-OCT-1996 (Rel. 34, Created)
 DR DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DR DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DR DE Adenylyl kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP
 DR DE transphosphorylase).
 DR GN AK2 OR ADK2.
 DR OS Homo sapiens (Human).
 DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR OC Mammalia; Eutheria; Primates; Cetacei; Hominidae; Homo.
 DR OX NCBI_TaxID=9606;
 DR RN [1]
 DR SEQUENCE FROM N.A.
 DR
 DR TISSUE=Liver;
 DR RX MEDLINE=9700211; PubMed=8843353;
 DR RA Lee J., Kim J.W., Lee I.A., Kang H.B., Choe Y.K., Lee H.G.,
 DR RA Lim J.S., Kim H.J., Park C., Choe I.S.;
 DR RT "Cloning and characterization of cDNA for human adenylyl kinase 2A.",
 DR RL Biochem. Mol. Biol. Int. 39:833-842(1996).
 DR RN [2].
 DR SEQUENCE FROM N.A.
 DR RX MEDLINE=98162934; PubMed=9504408;
 DR RA Lee Y., Kim J.W., Lee S.M., Kim H.J., Lee K.S., Park C., Choe I.S.;
 DR RT "Cloning and expression of human adenylyl kinase 2 isozymes: differential expression of adenylyl kinase 1 and 2 in human muscle
 DR RT tissues.", J. Biochem. 123:47-54(1998).
 DR RN [3].
 DR SEQUENCE FROM N.A.
 DR RC Strausberg R.;
 DR
 RA Noma T.;

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC 1- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC MAINTENANCE AND CELL GROWTH.
 CC -I- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -I- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Mitochondrial intermembrane space.
 CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; AK2A (SHOWN HERE) AND AK2B;
 CC ARE PRODUCED BY ALTERNATIVE SPlicing.
 CC -I- TISSUE SPECIFICITY: ABUNDANT IN HEART.
 CC -I- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; U39945; AAC2061.1;
 DR EMBL; U84371; AAC4190.1; -;
 DR EMBL; U54445; AAC13881.1; -;
 DR EMBL; BC009405; AAH09405.1; -;
 DR HSSP; P08166; IAK2.
 DR Gene; HGNC:362; AK2.
 DR MIM; 103020; -;
 DR InterPro; IPR000850; Adenylate_kin.
 DR Pfam; PF00406; adenylatekinase; 1.
 DR PRIMs; PR00094; ADENYLTKINASE.
 DR PRODOM; PP00657; Adenylate_kin; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW Transferase; Kinase; ATP-binding; Mitochondrion; Alternative splicing.
 FT INIT_MET 0 By SIMILARITY.
 FT NP_BIND 29 ATP (BY SIMILARITY).
 FT VARSPLIC 231 238 CKDLYMFI -> S (IN ISOFORM AK2B).
 SQ SEQUENCE 238 AA; 26346 MW; 34B3844F355EC3D1 CRC64;

 Query Match 68.2%; Score 60; DB 1; Length 238;
 Best Local Similarity 66.7%; Pred. No. 0.1;
 Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 LRAVILGPGCGKGT 17
 Db 15 IRAWVILGPGCGKGT 29

Search completed: April 24, 2003, 10:18:46
 Job time : 25 secs

OM protein - protein search, using sw model1	GenCore version 5.1.4_p5_4578		
Run on:	copyright (c) 1993 - 2003 CompuGen Ltd.		
	April 24, 2003, 10:17:37 ; Search time 43 Seconds		
	(without alignments)		
	40.242 Million cell updates/sec		
Title:	US-10-006-190-1_COPY_6_23		
Perfect score:	88		
Sequence:	1 RLLRAVIMGAPGSGKGT 18		
Scoring table:	BLOSUM62		
	Gapop 10.0 , Gapext 0.5		
Searched:	283224 seqs, 96134422 residues		
Total number of hits satisfying chosen parameters:	283224		
Minimum DB seq length:	0		
Maximum DB seq length:	2000000000		
Post-processing:	Minimum Match 0%		
	Maximum Match 100%		
	Listing first 45 summaries		
Database :	PIR 7.3:*		
	1: pir1:*		
	2: pir2:*		
	3: pir3:*		
	4: pir4:*		
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		
SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	84	95.5 227 2 J01945	nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3, mitochondrial - rat
2	84	95.5 227 2 A34442	N; Alternate names: GTP-AMP phosphotransferase AK3
3	77	87.5 223 1 KIHUA3	C; Species: Rattus norvegicus (Norway rat)
4	77	87.5 223 1 KIHUA3	C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
5	62	70.5 198 2 .BB2825	C; Accession: J01945
6	62	70.5 225 2 S23568	R; Tanabe, T.; Yamada, M.; Noma, T.; Kajii, T.; Nakazawa, A.
7	61	69.3 245 2 D71554	J. Biochem. 113, 200-207, 1993
8	60	68.2 215 2 G83184	A; Title: Tissue-specific and developmentally regulated expression of the genes encode
9	60	68.2 232 1 JC5893	A; Reference number: P00534; MUID: 93224500; PMID: 8468325
10	60	68.2 239 2 G02248	A; Accession: J01945
11	60	68.2 239 2 J01944	A; Molecule type: mRNA
12	60	68.2 248 2 S44766	A; Residues: 1-227 <TAN>
13	59	67.0 214 1 KIECA	A; Cross-references: DDBJ:D13062; MUID: 9220797; PID: 9150312
14	59	67.0 214 2 S70734	C; Superfamily: adenylylate kinase
15	59	67.0 214 2 C02255	C; Keywords: ATP; GTP; mitochondrial; nucleotide binding; P-loop; phosphotransferase
16	59	67.0 214 2 AG0378	F; 14-21/Region: nucleotide-binding motif A (P-loop)
17	59	67.0 214 2 AC0563	Query Match 95.5%; Score 84; DB 2; Length 227;
18	59	67.0 214 2 C85545	RESULT 2
19	59	67.0 214 2 G90694	Qy 1 RLLRAVIMGAPGSGKGT 17
20	59	67.0 215 2 S61841	Db 6 RLLRAVIMGAPGSGKGT 22
21	59	67.0 215 2 S61843	
22	59	67.0 215 2 E84986	
23	59	67.0 215 2 F81154	
24	59	67.0 234 2 B29792	
25	59	67.0 241 2 J50422	
26	57	64.8 205 2 S17070	
27	56	63.6 181 2 R87138	
28	56	63.6 181 2 T45390	
29	56	63.6 213 2 D86521	
ALIGNMENTS			
30	56	63.6 213 2 H72100	adenylate kinase C
31	56	63.6 214 2 I64062	adenylate kinase (
32	55	62.5 215 2 I40341	adenylate kinases
33	55	62.5 215 2 AB1777	adenylate kinase (
34	55	62.5 215 2 AC1401	adenylate kinases
35	54	61.4 70 2 PC4087	adenylate kinase (
36	54	61.4 176 2 G70658	probable arck prot
37	54	61.4 187 2 S77483	adenylate kinase (.
38	54	61.4 194 2 AD3349	adenylate kinase (
39	54	61.4 199 2 PE4230	adenylate kinase
40	54	61.4 205 2 S50007	adenylate kinase (
41	54	61.4 214 2 I64218	adenylate kinase (
42	54	61.4 218 2 S43016	adenylate kinase (
43	54	61.4 222 1 KIBYA	adenylate kinase (
44	53	60.2 177 2 H87205	probable adenylate
45	53	60.2 181 2 H70822	probable adenylate

FEBS Lett. 202, 303-308, 1986

A;Title: The complete primary structure of GTP-AMP phosphotransferase from beef heart mi

A;Reference number: B2825; PMID:3013690

A;Accession: A24201; MUID:86248102; PMID:3013690

A;Molecule type: Protein

A;Residues: 2-10,12-227 <TOM>

C;Genetics:

A;Gene: AK3

A;Introns: 5/1; 91/1; 148/3; 188/2

C;Superfamily: Adenylate kinase

C;Keywords: AMP; mitochondrion; nucleotide binding; P-loop; phosphotransferase

F;2-227/Product: GTP-AMP phosphotransferase

F;14-21/Region: nucleotide-binding motif A (P-loop)

Query Match 95.5%; Score 84; DB 2; Length 227;

R;Best local Similarity 94.4%; Pred. No. 0.00012; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RURAVIVGAPGSGKGT 18

Db 6 RLRAIMGAPGSGKGT 23

RESULT 3

KIUUA3

nucleoside-triphosphate-adenylate kinase (EC 2.7.4.10) 3 - human

N;Alternate names: adenylate kinase 3

C;Species: Homo sapiens (man)

C;Accession: A42820; S16380; S16381

R;Xu, G.; O'Connell, P.; Stevens, J.; White, R.

Geomics 13, 537-542, 1992

A;Title: Characterization of human adenylyl kinase 3 (AK3) cDNA and mapping of the AK3

A;Reference number: A42820; MUID:92347846; PMID:1639383

A;Molecule type: mRNA

A;Residues: 1-223 <XUG>

A;Cross-references: EMBL:X0673; NID:928576; PIDN:CAA43088.1; PID:928577; GB:S41502

A;Experimental source: frontal-cortex

A;Note: sequence extracted from NCBI backbone (NCBIN:109644, NCBIPI:109645)

C;Genetics:

A;Gene: GDB:AK3

A;Cross-references: GDB:118988; OMIM:103030

A;Map position: 9pter-9p13

C;Function:

A;Description: catalyzes the reversible phosphorylation of adenine monophosphate with nu

C;Preferred: adenylyl kinase

C;Keywords: AMP; mitochondrial matrix; mitochondrion; P-loop; Phosphotransferase

F;12-19/Region: nucleotide-binding motif A (P-loop) #status atypical

F;85-89/Region: nucleotide-binding motif B #status atypical

F;22,33,35,88/Active site: Cys, His, Ser, Asp #status predicted

Query Match 87.5%; Score 77; DB 1; Length 223;

R;Best local Similarity 83.3%; Pred. No. 0.0012; Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RLRAIMGAPGSGKGT 18

Db 4 KLRAVIVGAPGSGKGT 21

RESULT 4

BB825

adenylate kinase XF0275 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;ID: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000

C;Accession: B8825

R;Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82315; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: B8825

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-198 <SIM>

A;Cross-references: EMBL:AE003881; GB:AE003849; NID:9105093; PIDN:AAF83088.1; GSPPDB:GN

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrer

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.G.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Kuramae, E.E.; La

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A;Authors: Martins, E.M.F.; Matsukawa, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, S.

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tsukako, M.H.; Vallada, H.; van Sluys, M.A.; Verjovskl-Almeida, S.; Vettore, A.L.

A;Reference number: A59328

A;Contents: annotation

C;genetics:

A;Gene: XFO275

C;Superfamily: Adenylate kinase

Query Match 70.5%; Score 62; DB 2; Length 198;

R;Best local Similarity 68.8%; Pred. No. 0.13; Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LLRAVIVGAPGSGKGT 17

Db 11 LMRLVLLGPPGSGKGT 26

RESULT 5

S23568

adenylate kinase (EC 2.7.4.3) ADK2 - yeast (Saccharomyces cerevisiae)

N;Alternate names: PAK3 protein; protein YER170w

C;Species: Saccharomyces cerevisiae

C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 19-Jan-2001

C;Accession: S23568; JG1135; S50673

R;Schricke, R.; Magdolin, V.; Bandlow, W.

Mol. Gen. Genet. 233, 363-371, 1992

A;Title: A new member of the adenylyl kinase family in yeast: PAK3 is highly homolog

A;Reference number: S23568; MUID:92318888; PMID:1620094

A;Molecule type: DNA

A;Residues: 1-225 <SCH>

A;Cross-references: EMBL:X65126; NID:94096; PIDN:CAA46254.1; PID:94097

R;Cooper, A.J.; Friedberg, E.C.

Gene 11, 145-148, 1992

A;Title: A putative second adenylyl kinase-encoding gene from the yeast Saccharomyce

A;Reference number: JG1135; MUID:92267376; PMID:1587477

A;Accession: JC1135

A;status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-225 <COO>

A;Cross-references: GB:M7757; NID:9171045; PID:AAA34418.1; PID:9171046

R;Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A;Description: The sequence of S. cerevisiae cosmids 9163 and 9132.

A;Reference number: S50673

A;Accession: S50673

C;genetics:

A;Gene: SGD:ADK2; PAK3

A;Cross References: SGD:S0000972; MIPS:YER170w

A;Map position: 5R

A;Function:

A;Description: phosphotransferase

C;Superfamily: Adenylate kinase

C,Keywords: ATP; mitochondrion; nucleotide binding; P-loop; phosphotransferase
 F;21-28/Region: nucleotide-binding motif A (P-loop)

Query Match 70.5%; Score 62; DB 2; Length 225;

Best Local Similarity 73.3%; Pred. No. 0.15; Mismatches 1; Indels 0; Gaps 0;

Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVIMGAPGSGKGT 17
 ||:::||||| 11
 Db 15 LRULLLGAPGSGKGT 29

RESULT 6

D71554

probable adenylate cyclase - *Chlamydia trachomatis* (serotype D, strain UW3/CX)

C,Species: *Chlamydia trachomatis*

C,Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 24-Nov-1999

C,Accession: D71554

R,Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,

Science 282, 754-759, 1998

A,Title: Genome sequence of an obligate intracellular pathogen of humans: *Chlamydia trachomatis*

A,Reference number: A71570; MUID:99000809; PMID:9784136

A,Accession: D71554

A,Status: preliminary

A,Molecule type: DNA

A,Residues: 1-245 <ARN>

A,Cross-references: GB:AE001286; GB:AE001273; NID:93328516; PIDN: AAC67719.1; PID:9332852

A,Experimental source: serotype D, strain UW-3/CX

C,Genetics:

A,Gene: adk

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

adenylate kinase PA3686 [Imported] - *Pseudomonas aeruginosa* (strain PA01)
 C,Species: *Pseudomonas aeruginosa*

C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C,Accession: G83184

R,Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.;

Adan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, R.; Larbig, K.; Li, L.

; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A,Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pa

A,Reference number: A82950; MUID:20437337; PMID:10984043

A,Accession: G83184

A,Status: preliminary

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

C,Superfamily: adenylate kinase

A,Molecule type: DNA

A,Residues: 1-215 <STO>

A,Cross-references: GB:AE004788; GB:AE004091; NID:9949846; PIDN: AAC07074.1; GSPDB:GN|

A,Experimental source: strain PA01

C,Genetics:

A,Gene: adk; PA3606

RESULT 8

G83184

C;Accession: G02248
 R;Choe, T.
 Submitted to the EMBL Data Library, November 1995
 A;Reference number: H00907
 A;Accession: G02248
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-239 <CHO>
 A;Cross-references: EMBL:U39945; NID:g1209686; PIDN:AC52061.1; PID:g1209687
 A;Experimental source: tissue fetal liver
 C;Genetics:
 A;Gene: adk2
 C;Function:
 A;Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
 A;Note: magnesium required
 C;Superfamily: adenylyl kinase
 C;Keywords: alternative splicing; ATP; P-loop; phosphotransferase
 C;Keywords: nucleotide-binding motif A (P-Loop) #status atypical
 F;95-100/Region: nucleotide-binding motif A (P-Loop) #status atypical
 F;42-92/Disulfide bonds: #status predicted
 F;43, 99, 145/Active site: His, Asp, His #status predicted
 Best Local Similarity 68.2%; Score 60; DB 2; Length 239;
 Matches 10; Conservative 10; Mismatches 4; Indels 1; Gaps 0; -
 Qy 3 LRAVIMGARGSGKGT 17
 Qy ::||:|| ::||:|||
 Db 16 IRAVLLGPGGAGKGT 30

RESULT 11
 J01944
 adenylyl kinase (EC 2.7.4.3) 2, mitochondrial - rat .
 N;Alternate names: ATP-AMP phosphotransferase AK2
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 20-Jun-2000
 C;Accession: J01944
 R;Tanabe, T.; Yamada, M.; Noma, T.; Kajii, T.; Nakazawa, A.
 J. Biochem. 113, 200-207, 1993
 A;Title: Tissue-specific and developmentally regulated expression of the genes encoding
 A;Reference number: P05334; MUID:93224500; PMID:846825
 A;Accession: J01944
 A;Molecule type: mRNA
 A;Residues: 1-239 <TAN>
 C;Cross-references: DDBJ:D13061; NID:g220795; PIDN:BA02378.1; PID:g220796
 A;Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
 A;Note: magnesium required
 C;Superfamily: adenylyl kinase
 C;Keywords: ATP; mitochondrion; P-loop; phosphotransferase
 F;22-100/Region: nucleotide-binding motif A (P-loop) #status atypical
 F;42-92/Disulfide bonds: #status predicted
 F;43, 99, 145/Active site: His, Asp, His #status predicted
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 Best Local Similarity 66.7%; Pred. No. 0.31;
 Matches 10; Conservative 10; Mismatches 4; Indels 1; Gaps 0; -
 Qy 3 LRAVIMGARGSGKGT 17
 Qy ::||:|| ::||:|||
 Db 25 RGIRAFICPPGSGKGT 41

RESULT 12
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 adenylyl kinase (EC 2.7.4.3) [validated] - Escherichia coli (strain K-12)
 N;Alternate names: ATP-AMP transphosphorylase
 C;Species: Escherichia coli
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 01-Mar-2002
 C;Accession: A24275; S25734; A64778
 R;Brune, M.; Schumann, R.; Wittighofer, F.
 Nucleic Acids Res. 13, 7139-7151, 1985
 A;Title: Cloning and sequencing of the adenylyl kinase gene (adk) of Escherichia coli
 A;Reference number: A24275; MUID:86041903; PMID:2297739
 A;Accession: A24275
 A;Molecule type: DNA
 A;Residues: 1-214 <BRU>
 A;Cross-references: GB:X03038; NID:g40903; PIDN:CAA26840.1; PID:g40904
 A;Experimental source: K-12
 R;Miyamoto, K.; Nakahashi, K.; Nishimura, K.; Inokuchi, H.
 J. Mol. Biol. 219, 393-398, 1991
 A;Title: Isolation and characterization of visible light-sensitive mutants of Escherichia coli
 A;Reference number: S16118; MUID:91269316; PMID:2051480
 A;Accession: S25734
 A;Molecule type: DNA
 A;Status: translation not shown
 A;Cross-references: EMBL:D90259; NID:g285769; PIDN:BA14303.1; PID:g216516
 R;Blattner, F.R.; Blunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64778; MUID:97426517; PMID:9278503
 A;Accession: A64778
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-214 <BLAT>
 A;Cross-references: GB:AB000153; GB:U00096; NID:g1786671; PIDN:AACT3576.1; PID:g17866
 A;Experimental source: strain K-12, substrate MG1655
 R;Rose, T.; Brune, M.; Wittighofer, A.; Le Blay, K.; Surewicz, W.K.; Mantsch, H.H.;
 J. Biol. Chem. 266, 10781-10786, 1991
 A;Cross-references: GB:AB000153; GB:U00096; NID:g1786671; PIDN:AACT3576.1; PID:g17866
 A;Title: Structural and catalytic properties of a deletion derivative (delta-133-157)
 A;Reference number: A40519; MUID:9125071; PMID:2040598
 A;Contents: annotation; deletion mutant characterization
 A;Note: a construct lacking residues 133-157, corresponding to the insert found in la
 of maximum levels for wild type enzyme
 R;Berry, M.B.; Meador, B.; Bilderback, T.; Liang, P.; Glaser, M.; Phillips Jr., G.N.

Submitted to the Brookhaven Protein Data Bank, February 1994
 A; Reference number: A52276; PDB:1ANX
 A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 1-214
 C; Genetics:
 A; Gene: adk; p18A; draw
 A; Map position: 11 min
 C; Function:
 A; Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
 A; Note: magnesium required
 C; Superfamily: adenylylate kinase
 C; Keywords: ATP; P-loop; phosphotransferase
 F; 7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
 F; 80-85/Region: nucleotide-binding motif B #status atypical
 F; 30,84/Active site: Ser, Asp #status predicted

Query Match	Best Local Similarity	Score	DB	Length	Pred.	Mismatches	Conservative	Indels	Gaps
Qy 3 LRAVINGGAPGSKGT	67.0%	59	1	214	0.38	5	1	0	0
Db 1 MRLILGAPGAGKGT									

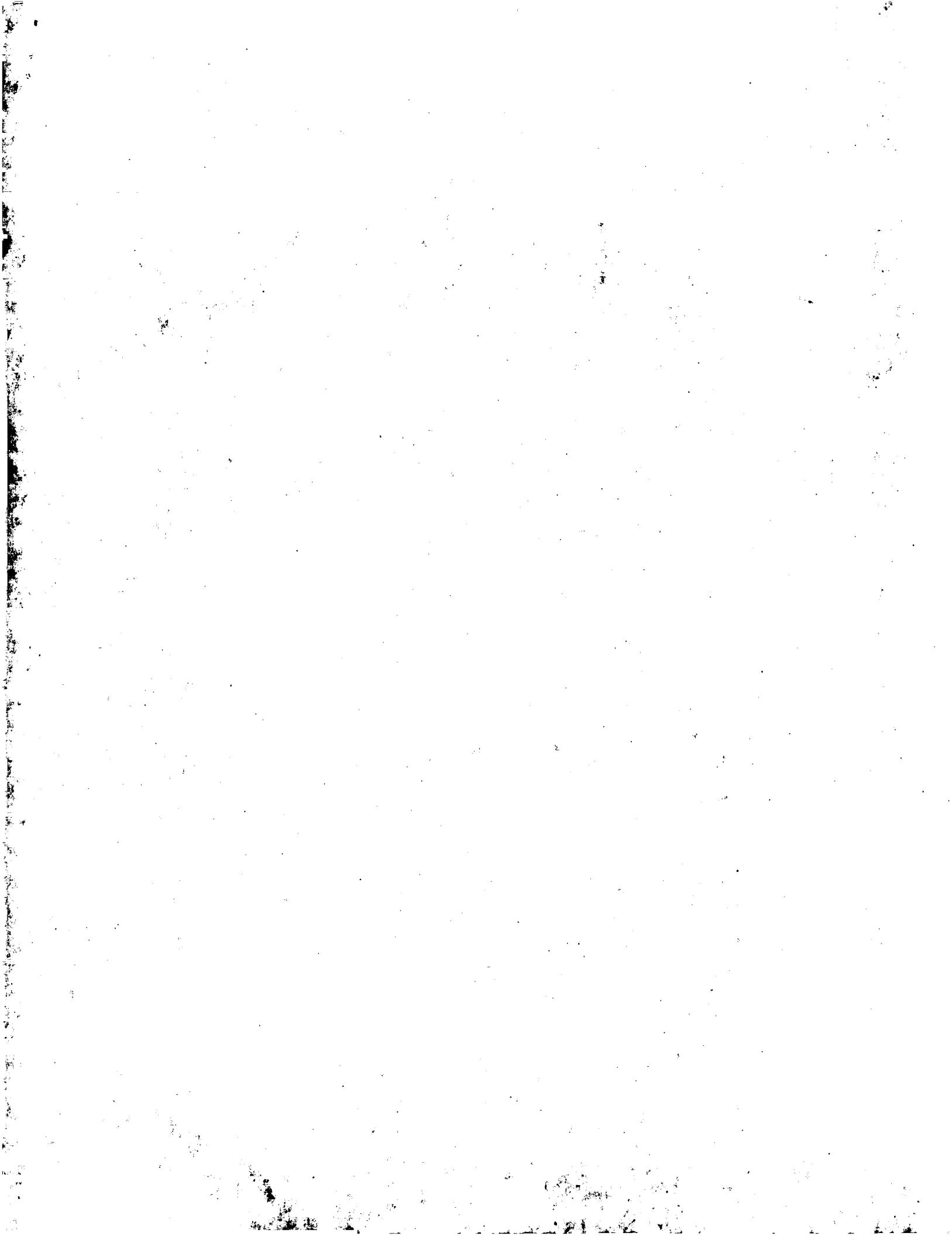
RESULT 14
 S70734
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 N; Alternative names: ATP-AMP transphosphorylase
 C; Species: *Yersinia enterocolitica*
 C; Accession: S70734; S51258
 C; Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
 R; Skurnik, M.; Venho, R.; Toivanen, P.; Al-Hendy, A.
 MOL: Microb. 17, 575-594, 1995
 A; Title: A novel locus of *Yersinia enterocolitica* serotype O:3 involved in lipopolysaccharide biosynthesis
 A; Reference number: S70734; MUID:96100456; PMID:8559076
 A; Accession: S70734
 A; Status: nucleic acid sequence not shown; translation not shown
 A; Molecule type: DNA
 A; Residues: 1-214 <SKU>
 A; Cross-references: EMBL:247767; NID:9633689; PIDN:CAA87696.1; PID:9633690
 A; Experimental source: strain 6471/76 serotype O:3
 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 C; Genetics:
 A; Gene: adk
 C; Function:
 A; Description: catalyzes reversible phosphorylation of AMP with ATP to form two ADP
 A; Note: magnesium required
 C; Superfamily: adenylylate kinase
 C; Keywords: ATP; P-loop; phosphotransferase
 F; 7-14/Region: nucleotide-binding motif A (P-loop) #status atypical
 F; 80-85/Region: nucleotide-binding motif B #status atypical
 F; 126/Active site: HIS #status predicted

Query Match	Best Local Similarity	Score	DB	Length	Pred.	Mismatches	Conservative	Indels	Gaps
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Db 1 MRLILGAPGAGKGT									

RESULT 15
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 C; Species: *Vibrio cholerae*
 C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C; Accession: C82255
 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Embley, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, E.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
 A; Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

Query Match	Best Local Similarity	Score	DB	Length	Pred.	Mismatches	Conservative	Indels	Gaps
Qy 3 LRAVINGGAPGSKGT	67.0%	59	2	214	0.08	5	1	0	0
Db 1 MRLILGAPGAGKGT									

Search completed: April 24, 2003, 10:20:18
 Job time : 44 secs



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GenCore version 5.1.4_p5_4578

Om protein - protein search, using sw model

Run on: April 24, 2003, 10:17:37 : Search time 15 seconds
(without alignments)

Sequence: 35.308 Million cell updates/sec

Title: US-10-006-190-1_COPY_6_23

Perfect score: 88

Sequence: 1 RLLRAYIMGAPGSGKGTV 18

Scoring table: BLOSUM62

Gappen 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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3: /cn2_6/ptodata/1/iaa/5A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cn2_6/ptodata/1/iaa/PCMU5_COMB.pep:*

6: /cn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	84	95.5	227	2	US-08-829-027-3
5	84	95.5	227	2	US-08-829-027-4
6	84	95.5	227	3	US-09-225-366-3
7	84	95.5	227	3	US-09-225-366-4
8	77	87.5	223	2	US-08-829-027-5
9	77	87.5	223	3	US-09-225-366-5
10	58	65.9	438	4	US-08-157-498B-37
11	52	59.1	222	0	US-09-134-001C-3289
12	50	56.8	197	2	US-08-879-561-5
13	49	55.7	194	2	US-08-879-561-11
14	49	55.7	194	2	US-08-879-561-12
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16	48	54.5	288	4	US-09-134-001C-4963
17	46	52.3	1463	1	US-08-157-005-3
18	46	52.3	1463	4	US-08-747-863-3
19	46	52.3	1463	4	US-09-865-864-3
20	45	51.1	283	4	US-09-222-939-2
21	45	51.1	2517	2	US-08-801-263A-5
22	45	51.1	2517	3	US-09-102-248-5
23	43	48.9	539	2	US-08-759-581B-20
24	43	48.9	539	4	US-09-304-711-20
25	43	48.9	539	4	US-09-281-20
26	43	48.9	1065	3	US-08-630-172-9
27	43	48.9	1065	4	US-09-375-419-9

RESULT 1

US-08-829-027-1

; sequence 1, Application US/08829027

Patent No. 5856160

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

APPLICANT: Shah, Purvi

TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYLATE KINASE

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADRESSE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

ZIP: 94304

COUNTRY: USA

COMPUTER READABLE FORM:

OPERATING SYSTEM: DOS Compatible

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/829,027

FILING DATE: Herewith

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PP-0256 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-555-0555

TELEFAX: 415-845-4165

TELEX:

IMMEDIATE SOURCE:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 227 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

LIBRARY: Consensus

CLONE: 2122022

Query Match Similarity: 100.0%; Score: 88; DB: 2; Length: 227; Best Local Similarity: 100.0%; Pred. No: 1.e-05; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 RLURAVINGAPGSGKGTV 18
 US-09-225-366-1
 Sequence 1, Application US/09225366
 ; Patent No. 6001624
 ; GENERAL INFORMATION:
 ; APPLICANT: Shah, Purvi
 ; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Innyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/225, 366
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/829, 027
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 REFERENCE/DOCKET NUMBER: PF-0256 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-4166
 TELEX:
 SEQUENCE FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 227 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Consensus
 CLONE: 2122022
 US-09-225-366-1

Query Match 100.0%; Score 88; DB 3; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05; Mismatches 0; Indels 0; Gaps 0;
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QY 1 RLURAVINGAPGSGKGTV 18
 US-09-225-366-1
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 ; Patent No. 6420526
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 186 Human Secreted Proteins
 ; FILE REFERENCE: P2002P1
 ; CURRENT APPLICATION NUMBER: US/09/149, 476
 ; CURRENT FILING DATE: 1998-09-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493

RESULT 2
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 ; Patent No. 6001624
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Innyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/225, 366
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/829, 027
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 REFERENCE/DOCKET NUMBER: PF-0256 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-4166
 TELEX:
 SEQUENCE FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 227 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: Consensus
 CLONE: 2122022
 US-09-225-366-1

EARLIER FILING DATE: 1998-03-06
 EARLIER APPLICATION NUMBER: 60/040, 162
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/040, 333
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 EARLIER APPLICATION NUMBER: 60/040, 626
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 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/043, 580
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 EARLIER FILING DATE: 1997-04-11
 EARLIER APPLICATION NUMBER: 60/048, 974
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/056, 886
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 877
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 889
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 893
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 870
 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 888
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 637
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 872
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 882
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 662
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 877
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 881
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 664
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 875
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 882
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 909
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 875
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 882
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 887
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 908
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 862
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 887
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056, 884
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/057, 669
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/049, 610
 EARLIER FILING DATE: 1997-06-13
 EARLIER APPLICATION NUMBER: 60/061, 060
 EARLIER FILING DATE: 1997-10-02

Query Match 100.0%; Score 88; DB 4; Length 227;
 Best Local Similarity 100.0%; Pred. No. 1;le-05; Mismatches 0;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 RLLRAVIMGAPGSKGTIV 18	1 1 1 1
Db	6 RLLRAVIMGAPGSKGTIV 23	1 1 1 1

RESULT 4
 US-08-829-027-3
 ; Sequence 3, Application US/08829027
 ; Patent No. 5856160
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLATE KINASE
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 CURRENT APPLICATION DATA: FastaSEQ for Windows Version 2.0
 APPLICATION NUMBER: US/08/829, 027
 FILING DATE: Hereworth
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 REFERENCE/DOCKET NUMBER: PF-0256 US
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 227 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 450312

US-08-829-027-3

Query Match Best Local Similarity 95.5%; Score 84; DB 2; Length 227;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RLLRAVINGAPGSGKGT 18
 Db 6 RLLRAVINGAPGSGKGT 22

RESULT 5 US-08-829-027-4

Sequence 4, Application US/08829027
 Patent No. 585160

GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Shah, Purvi
 TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLYLATE KINASE
 NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastaSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/225, 366
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/829, 027
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36, 749
 REFERENCE/DOCKET NUMBER: PF-0256 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 227 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 217576

US-09-225-366-3

Query Match Best Local Similarity 95.5%; Score 84; DB 3; Length 227;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 RLLRAVINGAPGSGKGT 18

||||| ||||| |||||
6 RLLRAATMGAPSGKGTV 23

RESULT 7
US-09-225-365-4
Sequence 4, Application US/09225366
; Patent No. 6001624
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLIATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829, 027
; FILING DATE: Herewich
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 35,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEFAX: 415-845-4166
; TELEPHONE: 415-855-0555
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0256 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 227 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 450312
; US-09-225-366-4

||||| |||||
Query Match 95.5%; Score 84; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLLRAATMGAPSGKGTV 18
Db 4 KLLRAVILGPPGSGKGTV 21

RESULT 8
US-08-829-027-5
; Sequence 5, Application US/08829027
; Patent No. 585660
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL MITOCHONDRIAL ADENYLIATE KINASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225, 366
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/829, 027
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.

||||| |||||
Query Match 95.5%; Score 84; DB 3; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RLLRAVILGPPGSGKGTV 17
Db 6 RLLRAVILGPPGSGKGTV 22

REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0256 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 223 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 28577
 US-09-225-366-5

Query Match 87.5%; Score 77; DB 3; Length 223;
 Best Local Similarity 83.3%; Pred. No. 0.0044; 1; Indels 0; Gaps 0;
 Matches 15; Conservative 2; Mismatches 1; Db 113 RVLRLVILGAPNACKSTL 130

RESULT 10
 US-08-915-498B-37
 Sequence 37, Application US/08915498B
 Patent No. 6132054
 GENERAL INFORMATION:
 APPLICANT: James R. Iupski, Robert A. Britton, Donald L.
 APPLICANT: Court and Bradford S. Powell
 TITLE OF INVENTION: Methods of Screening for Agents that
 TITLE OF INVENTION: Delay a Cell Cycle and Compositions Comprising ERA and an Anal
 TITLE OF INVENTION: of Wild-Type ERA
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WORDPERFECT FOR WINDOWS 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/915,498B
 FILING DATE: August 20, 1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/023,353
 FILING DATE: August 20, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Lori Y. Beardell
 REGISTRATION NUMBER: 34,293
 REFERENCE/DOCKET NUMBER: BYLR-0037
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 569-3439
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 438
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-915-498B-37

Query Match 65.9%; Score 58; DB 4; Length 438;

RESULT 11
 US-09-134-001C-3289
 Sequence 329, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucette-Stamm et al
 PATENT NO. 6380370
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 3289
 LENGTH: 222
 TYPE: PRT
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3289

RESULT 12
 US-08-879-561-5
 Sequence 5, Application US/08879561
 Patent No. 581482
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Hawkins, Phillip R.
 APPLICANT: Guegler, Karl J.
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/879,561
 FILING DATE: Herewith
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0325 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-845-0555
 TELEFAX: 415-845-4166
 TELX:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: CORNOT02
 CLONE: 1484821
 US-08-879-561-5

Query Match Similarity 56.0%; Score 50; DB 2; Length 197;
 Best Local Similarity 81.8%; Pred. No. 3-3; Mismatches 1; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 IMGAPGSGKGT 17
 Db 16 IIGGPGSGKGT 26

RESULT 13
 US-08-879-561-11
 Sequence 11, Application US/08879561
 Patent No. 5817482
 GENERAL INFORMATION:
 APPLICANT: Bandman, Olga
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Hawkins, Phillip R.
 APPLICANT: Guebler, Karl J.
 APPLICANT: Corley, Neil C.
 TITLE OF INVENTION: DISEASE RELATED NUCLEOTIDE KINASES
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 ZIP: 94304
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/879,561
 FILING DATE: Herewith
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0325 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELX:
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 194 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-879-561-12

Query Match Similarity 72.7%; Pred. No. 4-5;
 Best Local Similarity 72.7%; Pred. No. 4-5; Mismatches 1; Indels 0; Gaps 0;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 IMGAPGSGKGT 17
 Db 14 WVGGPGSGKGT 24

RESULT 15
 US-09-222-939-17
 Sequence 17, Application US/09222939
 Patent No. 6372448
 GENERAL INFORMATION:
 APPLICANT: Fritz, Christian
 APPLICANT: Youngman, Phillip
 APPLICANT: Guzman, Luz-Marie
 TITLE OF INVENTION: USE OF YLQF, YQEG, YVHQ, YERL, AND YSXC, ESSENTIAL BACTERIAL

Query Match 55.7%; Score 49; DB 2; Length 194;

US-08-879-561-11

US-08-879-561-5

Query Match 55.7%; Score 49; DB 2; Length 194;

US-09-222-939-17

Sequence 17, Application US/09222939

Patent No. 6372448

GENERAL INFORMATION:

APPLICANT: Fritz, Christian

APPLICANT: Youngman, Phillip

APPLICANT: Guzman, Luz-Marie

TITLE OF INVENTION: USE OF YLQF, YQEG, YVHQ, YERL, AND YSXC, ESSENTIAL BACTERIAL

TITLE OF INVENTION: GENES AND POLYPEPTIDES
FILE REFERENCE: 07334/111001
CURRENT APPLICATION NUMBER: US/09/7222, 939
CURRENT FILING DATE: 1998-12-30
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 17
LENGTH: 282
TYPE: PRY
ORGANISM: *Bacillus subtilis*
US-09-222-939_17

Query Match 54 5%; Score 48; DB 4; Length 282;
Best Local Similarity 50.0%; Pred. No. 9.2;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RLLRAVIMGAPGSSKGTV 18
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Db 119 RAIRALITGIPNVEKSTL 136

Search completed: April 24, 2003, 10:20:40
Job time : 16 secs

GenCore version 5.1.4-p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
Run on: April 24, 2003, 10:17:37 : Search time 35 Seconds

(without alignments)
68.529 Million cell updates/sec

Title: US-10-006-190-1_COPY_6_23
Perfect score: 88
Sequence: 1 RLLRAVIMGAPSGKGTV 18
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /\$IDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1981.DAT:*
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- 6: /\$IDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1985.DAT:*
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- 11: /\$IDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1990.DAT:*
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- 20: /\$IDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /\$IDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /\$IDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /\$IDS2/gcdata/geneseq/geneseq/geneseq-emb1/AA2002.DAT:*

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	88	100	0 227 19 AAW81:01	Human mitochondrial Human secreted protein
2	88	100	0 227 19 AAW74:07	Human mitochondrial Human polypeptides
3	88	100	0 227 21 AAB124:40	Human protein secreted Human protein secreted Human adenylyl kinase
4	88	100	0 227 22 AAM38:99	Human polypeptides
5	88	100	0 227 22 AAB92:87	Human protein secreted Human protein secreted Human adenylyl kinase
6	88	100	0 227 22 AAB93:66	Human polypeptides
7	88	100	0 227 22 AAB93:87	Human polypeptides
8	88	100	0 227 22 AAB85:88	Human polypeptides
9	88	100	0 239 22 ABB122:26	Human polypeptides
10	88	100	0 239 22 AAM40:85	Human polypeptides

RESULT 1	
ID	AAB81101
AC	AAB81101 standard; Protein; 227 AA.
XX	
XX	AAB81101;
XX	
DT	29-JAN-1999 (first entry)
XX	
DE	Human mitochondrial adenylylate kinase protein.
XX	
KW	Human; mitochondrial; adenylylate kinase; therapeutic;
KW	neurological disorder; Alzheimer; Huntington; epilepsy; car-
KW	neural; inflammation; immune.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
MISC-difference	182
FT	/note= "Xaa is unspecified, encoded by NCA"
MISC-difference	185
FT	/note= "Xaa is unspecified, encoded by GNAW"
XX	
PN	W09844124-A1.
XX	
PD	08-OCT-1998.
XX	
PF	30-MAR-1998; 98W0-US06249.
XX	
PR	31-MAR-1997; 97US-00329027.
XX	
PA	(INCYT-) INCYTE PHARM INC.
XX	
PI	Hillman JL, Shah P;

Score, N , is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

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updates/sec	15	70	79.5	214	21	AAU53619
	16	64	72.7	203	22	AAU2464
	17	62	70.5	335	22	ABG33968
	18	61	69.3	245	20	ABV37077
	19	60	68.2	106	21	AAG01367
	20	60	68.2	215	22	AAU63439
	21	60	68.2	232	20	AAU7257
	22	60	68.2	237	23	ABP1753
	23	60	68.2	238	22	ABG19263
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	26	59	67.0	214	22	AAU8124
	27	59	67.0	64.0	22	ABG26095
	28	58	65.9	86	22	AGG19570
	29	58	65.9	158	21	AAG02190
	30	58	65.9	342	21	AAB5190
	31	58	65.9	437	20	AYV8919
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	34	58	65.9	438	22	ABG25620
	35	58	65.9	443	22	AM02084
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	37	57	64.8	237	22	AB59655
	38	56	63.6	214	22	AAU35415
	39	56	63.6	224	22	AAU66334
	40	56	63.6	224	22	AAU7231
	41	55	62.5	74	22	ABBA3756
	42	55	62.5	74	22	AM77489
	43	55	62.5	74	22	AM11416
	44	55	62.5	74	22	AM37653
	45	55	62.5	74	23	ABG46511
						ALIGNMENTS
RESULT 1						
AAW81101						
ID	AAW81101	standard;	Protein;	227 AA.		
XX						
AC	AAW81101;					
XX						
DT	29-JAN-1999	(first	entry)			
XX						
DE	Human mitochondrial adenylate kinase prote					
XX						
KW	Human; mitochondrial; adenylylate kinase; the					
KW	neurological disorder; Alzheimer; Huntington					
KW	neural; inflammation; immune.					
XX						
OS	Homo sapiens.					
XX						
FH	Key	Location/Qualifiers				
FT	Misc-difference	182				
FT		/note= "Xaa is unspecified				
FT	Misc-difference	185				
FT		/note= "Xaa is unspecified				
XX						
PN	W09844124-A1.					
XX						
FT	08-OCT-1998.					
XX						
PF	30-MAR-1998;	98WO-US06249.				
XX						
PR	31-MAR-1997;	97US-0829027.				
XX						
PA	(INCY-) INCYTE PHARM INC.					
XX						
PI	Hillman JL, Shah P;					
Description	e to have a					
	t being printed,					
	ution.					
Human mitochondria						
Human secreted pro						
Human mitochondrial						
Human Polypeptide						
Human protein sequ						
Human protein sequ						
Human adenylate ki						
Human secreted pro						
Human polypeptide						

XX	WPI; 1998-557119/47.	PR	11-APR-1997;	97US-0043576.
DR	N-PSDB; AAV68223.	PR	11-APR-1997;	97US-0043578.
PT	Human mitochondrial adenylate kinase, HMAK - useful e.g. to treat neurological disorders such as Alzheimer's and screen for antagonists for treatment of cancer or immunological disorders	PR	11-APR-1997;	97US-0043669.
PT	neurological disorders such as Alzheimer's and screen for antagonists for treatment of cancer or immunological disorders	PR	11-APR-1997;	97US-0043670.
XX	Claim 5; Fig 1; 63pp; English.	PR	11-APR-1997;	97US-0043672.
PS		PR	11-APR-1997;	97US-0043674.
XX	The human mitochondrial adenylate kinase (HMAK) protein of 227 amino acids) can be administered therapeutically, especially by expressing, encoding polypeptides, to treat neurological disorders e.g. Alzheimer's disease, Huntington's disease, epilepsy. It can be combined with a suitable carrier in pharmaceutical compositions which can be administered to treat such disorders. HMAK was shown to have chemical and structural homology with adenylate kinase isozyme 3 (AK3) from cow, rat and human (92, 91 and 57 % identity respectively) and was expressed in e.g. cancerous tissues, brain and neural tissues and tissues involved in inflammation and the immune response. Increased activity or expression was proposed to be associated with cancer and immunological disorders, and decreased activity/expression with the development of neurological disorders. Products of the above invention may be used in the diagnosis and treatment of the above diseases and disorders.	PR	23-MAY-1997;	97US-0047501.
SQ	Sequence 227 AA:	PR	23-MAY-1997;	97US-0047502.
	Query Match 100.0%; Score 88; DB 19; Length 227; Best Local Similarity 100.0%; Pred. No. 0.0001; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	PR	23-MAY-1997;	97US-0047503.
QY	1 RLLRAVINGAPSGSGKTV 18	PR	23-MAY-1997;	97US-0047582.
Db	6 RLLRAVINGAPSGSGKTV 23	PR	23-MAY-1997;	97US-0047583.
RESULT 2		PR	23-MAY-1997;	97US-0047584.
AAW74787		PR	23-MAY-1997;	97US-0047585.
ID AAW74787	standard; Protein; 227 AA.	PR	23-MAY-1997;	97US-0047586.
AC		PR	23-MAY-1997;	97US-0047587.
XX		PR	23-MAY-1997;	97US-0047588.
AAW74787;		PR	23-MAY-1997;	97US-0047589.
XX		PR	23-MAY-1997;	97US-0047590.
19-JAN-1999 (first entry)		PR	23-MAY-1997;	97US-0047591.
DT		PR	23-MAY-1997;	97US-0047592.
XX		PR	23-MAY-1997;	97US-0047593.
DE	Human secreted protein encoded by gene 58 clone HHEHN61.	PR	23-MAY-1997;	97US-0047594.
XX		PR	23-MAY-1997;	97US-0047595.
KW	Human; secreted protein; testis; tumour; foetal brain tissue; fusion protein; cancer; central nervous system; seizure; diagnosis; neurodegenerative disease.	PR	23-MAY-1997;	97US-0047596.
KW		PR	23-MAY-1997;	97US-0047597.
XX		PR	23-MAY-1997;	97US-0047598.
OS	Homo sapiens.	PR	23-MAY-1997;	97US-0047599.
XX		PR	23-MAY-1997;	97US-0047600.
PN	W09839448-A2.	PR	23-MAY-1997;	97US-0047601.
XX		PR	23-MAY-1997;	97US-0047612.
PO	11-SEP-1998.	PR	23-MAY-1997;	97US-0047613.
XX		PR	23-MAY-1997;	97US-0047614.
PF	06-MAR-1998; 98WO-US04493.	PR	23-MAY-1997;	97US-0047615.
XX		PR	23-MAY-1997;	97US-0047616.
PR	02-OCT-1997; 97US-0061060.	PR	23-MAY-1997;	97US-0047618.
PR	07-MAR-1997; 97US-003621.	PR	23-MAY-1997;	97US-0047624.
PR	07-MAR-1997; 97US-004061.	PR	23-MAY-1997;	97US-0047632.
PR	07-MAR-1997; 97US-004062.	PR	06-JUN-1997;	97US-0047633.
PR	07-MAR-1997; 97US-004063.	PR	13-JUN-1997;	97US-0047634.
PR	07-MAR-1997; 97US-004064.	PR	08-JUL-1997;	97US-0051925.
PR	07-MAR-1997; 97US-004065.	PR	16-JUL-1997;	97US-0052874.
PR	07-MAR-1997; 97US-004066.	PR	18-AUG-1997;	97US-0047635.
PR	07-MAR-1997; 97US-004067.	PR	22-AUG-1997;	97US-0056630.
PR	07-MAR-1997; 97US-004068.	PR	22-AUG-1997;	97US-0056631.
PR	07-MAR-1997; 97US-004069.	PR	22-AUG-1997;	97US-0056632.
PR	07-MAR-1997; 97US-004070.	PR	22-AUG-1997;	97US-0056633.
PR	07-MAR-1997; 97US-004071.	PR	22-AUG-1997;	97US-0056634.
PR	07-MAR-1997; 97US-004072.	PR	22-AUG-1997;	97US-0056635.
PR	07-MAR-1997; 97US-004073.	PR	22-AUG-1997;	97US-0056637.
PR	07-MAR-1997; 97US-004074.	PR	22-AUG-1997;	97US-0056662.
PR	07-MAR-1997; 97US-004075.	PR	22-AUG-1997;	97US-0056664.
PR	07-MAR-1997; 97US-004076.	PR	22-AUG-1997;	97US-0056845.
PR	07-MAR-1997; 97US-004077.	PR	22-AUG-1997;	97US-0056862.
PR	07-MAR-1997; 97US-004078.	PR	22-AUG-1997;	97US-0056864.
PR	07-MAR-1997; 97US-004079.	PR	22-AUG-1997;	97US-0056872.
PR	07-MAR-1997; 97US-004080.	PR	22-AUG-1997;	97US-0056874.
PR	07-MAR-1997; 97US-004081.	PR	22-AUG-1997;	97US-0056875.
PR	07-MAR-1997; 97US-004082.	PR	22-AUG-1997;	97US-0056876.
PR	07-MAR-1997; 97US-004083.	PR	22-AUG-1997;	97US-0056877.
PR	07-MAR-1997; 97US-004084.	PR	22-AUG-1997;	97US-0056878.
PR	07-MAR-1997; 97US-004085.	PR	22-AUG-1997;	97US-0056879.
PR	07-MAR-1997; 97US-004086.	PR	22-AUG-1997;	97US-0056880.
PR	07-MAR-1997; 97US-004087.	PR	22-AUG-1997;	97US-0056881.
PR	07-MAR-1997; 97US-004088.	PR	22-AUG-1997;	97US-0056882.
PR	07-MAR-1997; 97US-004089.	PR	22-AUG-1997;	97US-0056884.
PR	11-APR-1997; 97US-004312.	PR	22-AUG-1997;	97US-0056886.
PR	11-APR-1997; 97US-004313.	PR	22-AUG-1997;	97US-0056887.
PR	11-APR-1997; 97US-004314.	PR	22-AUG-1997;	97US-0056888.
PR	11-APR-1997; 97US-0043568.	PR	22-AUG-1997;	97US-0056889.
PR	11-APR-1997; 97US-0043669.	PR	22-AUG-1997;	97US-0056890.

PR 22-AUG-1997; 97US-0056893. PF 28-SEP-1998; 98CN-0119439.
 PR 22-AUG-1997; 97US-005694. XX
 PR 22-AUG-1997; 97US-005693. PR 28-SEP-1998; 98CN-0119439.
 PR 22-AUG-1997; 97US-005698. XX
 PR 22-AUG-1997; 97US-0056909. PA (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
 PR 22-AUG-1997; 97US-0056910. XX
 PR 22-AUG-1997; 97US-0056911. PT Yu L, Zhao Y, Bi A;
 PR 05-SEP-1997; 97US-0056750. XX
 PR 05-SEP-1997; 97US-0057669. DR WPI; 2000-400718/35.
 PR 05-SEP-1997; 97US-0057761. DR N-PSDB; AAA60582.
 PR 12-SEP-1997; 97US-0058785. XX
 PA (HUMA-) HUMAN GENOME SCI INC. PR Preparation of human mitochondrial matrix GTP : AMP phosphotransferase,
 XX PT its encode sequence.
 PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA; XX
 PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS; XX
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA; XX
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z; XX
 XX WPI; 1998-506364/43. DR N-PSDB; AAA59568.
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode XX
 PT useful for diagnosis and treatment of e.g. cancers, neurological XX
 PT disorders, immune diseases, inflammation or blood disorders XX
 XX
 PS Claim 1; Page 575-576; 721pp; English. XX
 XX
 CC This sequence represents a secreted human protein encoded by the nucleic XX
 CC acid molecule designated Gene 58 from the human cDNA clone HHFHNG1 (deposited as clone ATCC 97899 and ATCC 209045). XX
 CC The gene can be used to generate fusion proteins by linking to the gene XX
 CC stability of the fused protein as compared to the human protein only. XX
 CC The invention relates to 186 novel genes and their fragments (nucleic XX
 CC acid sequences: AAW74731-W74736) which are useful for preventing, treating or ameliorating medical XX
 CC conditions e.g. by protein or gene therapy. Also, pathological XX
 CC conditions can be diagnosed by determining the amount of the new XX
 CC polypeptides in a sample or by determining the presence of mutations in XX
 CC the new polynucleotides. Specific uses are described for each of the 186 XX
 CC polynucleotides, based on which tissues they are most highly expressed in XX
 CC (see AAV55511 for described uses). XX
 SQ Sequence 227 AA; XX
 PT Best Local Similarity 100.0%; Score 88; DB 21; Length 227; XX
 PT Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; XX
 Oy 1 RLLRAVIMGAPGSGKGTIV 18 DB 6 RLLRAVIMGAPGSGKGTIV 23
 XX
 RESULT 4 Query Match 100.0%; Score 88; DB 21; Length 227; XX
 ID AAM38899 standard; Protein: 227 AA. XX
 XX
 AC AAM38899; XX
 DT 22-OCT-2001 (first entry) XX
 DE Human polypeptide SEQ ID NO 2044. XX
 KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; XX
 KW peripheral nervous system; neuropathy; central nervous system; CNS; XX
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; XX
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; XX
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammatory; XX
 KW leukaemia. XX
 OS Homo sapiens. XX
 PN WO200153312-A1. XX
 PD 26-JUL-2001. XX
 XX
 RESULT 3 PF 26-DEC-2000; 2000WO-US34263. XX
 ID AAB12440 standard; Protein: 227 AA. XX
 XX
 AC AAB12440; XX
 DT 20-OCT-2000 (first entry) XX
 DE Human mitochondrial GTP:AMP phosphotransferase SEQ ID NO:4. XX
 KW Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide. XX
 OS Homo sapiens. XX
 PN CN1249340-A. XX
 PD 05-APR-2000. XX
 XX
 PA (HYSE-) HYSEQ INC. XX
 PT Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D; XX
 PT Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J; XX
 PT Zhao QA, Zhou P, Goodrich R, Drmanac RT; XX
 DR WPI; 2001-442253/47.

DR N-PSDB: AAI58055.

PS Novel nucleic acids and polypeptides, useful for treating disorders

XX such as central nervous system injuries -

PT

XX Example 3: SEQ ID NO 2044: 10078pp; English.

The invention relates to human nucleic acids (AN157798-AA161369) and the encoded polypeptides (ANM8642-ANM42213) with nootropic, immunosuppressant and cytostatic activity. The Polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis and Shy-Drager syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

XX Sequence 227 AA:

Query Match 100.0%; Score 88; DB 22; Length 227; Best Local Similarity 100.0%; Pred. No. 0.0001; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLRAVINGAPGSGKGT 18
Db 6 RLLRAVINGAPGSGKGT 23

RESULT 5

ID AAB92887 standard; Protein: 227 AA.

XX AAB92887;

AC

DT

26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:11492..

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

OS

Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-0116126.

XX

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX

(HELI-) HELIX RES INST.

XX

PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI: 2001-318749/34.

PS Claim 8; SEQ ID 11492; 253JPP + CD ROM; English.

XX The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH1842 represent human cDNA sequences; AAB2446 to AAB5893 represent human amino acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.

XX Sequence 227 AA;

Query Match 100.0%; Score 88; DB 22; Length 227; Best Local Similarity 100.0%; Pred. No. 0.0001; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLLRAVINGAPGSGKGT 18
Db 6 RLLRAVINGAPGSGKGT 23

RESULT 6

ID AAB93066 standard; Protein: 227 AA.

XX AAB93066;

AC

DT

26-JUN-2001 (first entry)

DE Human protein sequence SEQ ID NO:11883.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

OS

Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-0116126.

XX

PR 29-JUL-1999; 99JP-0248036.

PR 27-AUG-1999; 99JP-0300253.

PR 11-JAN-2000; 2000JP-0118776.

PR 02-MAY-2000; 2000JP-0183767.

PR 09-JUN-2000; 2000JP-0241899.

XX

(HELI-) HELIX RES INST.

XX

PA Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI: 2001-318749/34.

PS Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.

XX
PS Claim 8; SEQ ID 11883; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH0166 to AAH13628 and
CC AAH1633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB9593 represent human amino acid sequences; and AAH13629 to AAH13632
CC of the present invention.

XX
Sequence 227 AA;

SQ

Query Match 100.0%; Score 88; DB 22; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;

Qy 1 RLLRAVIMGAPGSGKTV 18
6 RLLRAVIMGAPGSGKTV 23

RESULT 7
AAB93487
ID AAB93487 standard; Protein; 227 AA.
XX
AC AAB93487;
XX
DT 26-JUN-2001 (first entry)
DE Human protein sequence SEQ ID NO:12786.

XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS Homo sapiens.
XX
PN EP1074617-A2.
XX
PD 07-FEB-2001.
XX
PF 28-JUL-2000; 20000EP-0116126.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-030253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-018376.
PR 09-JUN-2000; 2000JP-0241899.
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.

XX
PS Claim 8; SEQ ID 12786; 2537pp + CD ROM; English.
XX
CC The present invention describes primer sets for synthesising 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC 5'-end sequence/3'-end sequence is selected from those defined in
CC the specification. The primer sets can be used in antisense therapy and
CC in gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH0166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC AAB9593 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.

XX
Sequence 227 AA;

SQ

Query Match 100.0%; Score 88; DB 22; Length 227;
Best Local Similarity 100.0%; Pred. No. 0.0001; Mismatches 0;
Matches 18; Conservative 0; Indels 0; Gaps 0;

Qy 1 RLLRAVIMGAPGSGKTV 18
6 RLLRAVIMGAPGSGKTV 23

RESULT 8
AAB8585
ID AAB8585 standard; Protein; 227 AA.
XX
AC AAB8585;
XX
DT 30-NOV-2001 (first entry)
DE Human adenylylate kinase 3 (AK3)-like protein.
XX
KW Adenylylate kinase 3-like protein; AK3-like protein; AK3; cell morphology;
KW MELAS; central nervous system disorder; epilepsy; skeletal muscle;
KW muscle disease; electron transfer disorder; leber disease; human;
KW diabetes mellitus; Pearson disease; Parkinson's disease.
XX
OS Homo sapiens.
XX
PN WO200109346-A1.
XX
PD 08-FEB-2001.
PF 28-JUL-2000; 2000WO-JP05066.
XX
PR 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-030253.
PR 18-OCT-1999; 99US-0159550.
PR 11-JAN-2000; 2000JP-0118776.
PR 17-FEB-2000; 2000US-0183322.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Hayashi K, Saito K, Yamamoto J, Ishii S;
PI Sugiyama T, Wakamatsu A, Nagai K, Otsuki T, Ihara S, Nakae H;
PI Nishikawa T, Kimura K;
XX

WPI: 2001-564737/63.
DR
N-PSDB; AAH47197.

PT
New gene encoding an adenylyl kinase 3-like protein, and the protein and antibodies to it, useful for diagnosis of brain disease e.g.

PT
epilepsy; muscle disease, genetic disorder, diabetes

PS
Claim 1: Page 34-35; 41pp; Japanese.

XX
The invention relates to a cDNA (clone C-NP2RP2000329) encoding a novel adenylyl kinase 3 (AK3)-like protein. C-NP2RP2000329 has functions of converting extracellular signals into intracellular signals and changing cell morphology. The AK3-like protein, polynucleotides and antibodies are useful in the investigation of diseases such as MEAS (cerebral accident condition with hyperlacticacidemia), central nervous system disorder, epilepsy, skeletal muscle conditions, muscle disease, electron transfer disorders, leber disease, diabetes mellitus, peason disease, Parkinson's disease, metabolism disorders and treatment agents. They are useful for developing diagnostics and treatment agents. The present sequence represents the human AK3-like protein of the invention.

CC
Sequence 227 AA;

Query Match 100.0%; Score 88; DB 22; Length 227; Best local Similarity 100.0%; Pred. No. 0.0001; Mismatches 18; Conservative 0; Indels 0; Gaps 0;

Qy 1 RLRRAVINGAPGSGKGTV 18

Db 6 RLRRAVINGAPGSGKGTV 23

RESULT 9

ABB12326 ID ABB12326 standard; Peptide; 239 AA.

AC ABB12326;
XX
DT 11-JAN-2002 (first entry)

DE Human secreted protein homologue, SEQ ID NO:2696.

XX
Human; cytokine; cell proliferation; cell differentiation; growth factor; haemopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis; proliferation; metastasis; cancer; tumour; haemopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.

OS Homo sapiens.

XX
WO200151188-A2.

XX
PD 09-AUG-2001.

XX
05-FEB-2001; 2001WO-US03800.

XX
03-FEB-2000; 2000WS-0396914.

PR 27-APR-2000; 2000WS-0560875.

XX
(HYSE-) HYSEQ INC.

XX
Tang YT, Liu C, Drmanac RT;

XX
WPI; 2001-457740/49.

DR
N-PSDB; ABA09570.

XX
Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject

e.g. arthritis and cancer

PT
Claim 20: Page 333; 1963PP; English.

XX
Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB08225-AB09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide or the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may have various activities, including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; haemopoiesis, regulatory activity; tissue growth activity; haemostatic or thrombolytic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis. Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and repair (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders. Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.

CC
Sequence 239 AA;

Query Match 100.0%; Score 88; DB 22; Length 239; Best local Similarity 100.0%; Pred. No. 0.0001; Mismatches 18; Conservative 0; Indels 0; Gaps 0;

Qy 1 RLRRAVINGAPGSGKGTV 18

Db 18 RLRRAVINGAPGSGKGTV 35

RESULT 10
AAM40685 ID AAM40685 standard; Protein; 239 AA.

AC AAM40685;
XX
DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 5616.

XX
Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia.

OS HOMO sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PR 26-DEC-2000; 2000WO-US54263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 XX
 PR 25-APR-2000; 2000US-05231.
 XX
 PR 09-JUL-2000; 2000US-0598042.
 XX
 PR 19-JUL-2000; 2000US-0620312.
 XX
 PR 03-AUG-2000; 2000US-0653450.
 XX
 PR 14-SEP-2000; 2000US-0662191.
 XX
 PR 19-OCT-2000; 2000US-0663036.
 XX
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSEB-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xie AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
 XX
 PS Example 2: SEQ ID NO 5616: 10078PP; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AA138642-AA142213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed specification.
 XX
 SQ Sequence 239 AA;
 Query Match 100.0%; Score 88; DB 22; Length 239;
 Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0;
 Qy 1 RLLRAVIMGAPGSGKGT 18
 Db 18 RLLRAVIMGAPGSGKGT 35
 RESULT 11
 AAG73865
 ID AAG73865 standard; Protein; 256 AA.
 XX
 AC AAG73865;
 XX
 DT 03-SEP-2001 (first entry)
 XX
 DE Human colon cancer antigen protein SEQ ID NO:4629.
 XX
 KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma.
 XX
 OS Homo sapiens.

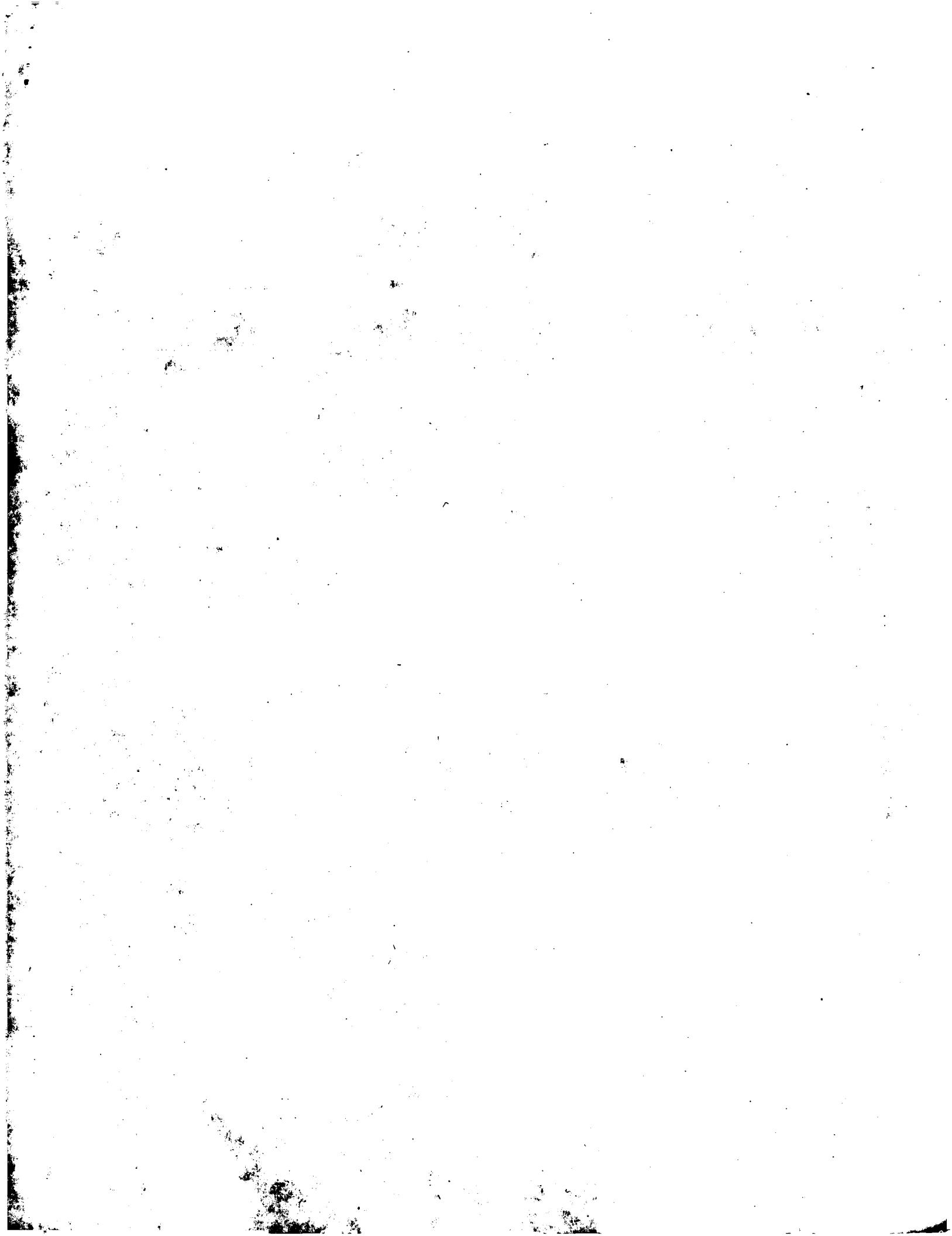
XX
 PN WO200122920-A2.
 XX
 PD 05-APR-2001.
 XX
 PR 28-SEP-2000; 2000WO-US26524.
 XX
 PR 29-SEP-1999; 99US-0157137.
 XX
 PR 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX
 DR WPI: 2001-235357/24.
 DR N-PSDB; AAH33296.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 11: Page 6430-6431; 9803PP; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG7788 represent human colon cancer-associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate P expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patient's own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB7789 represent sequences used in the exemplification of the present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 256 AA;
 Query Match 100.0%; Score 88; DB 22; Length 256;
 Best Local Similarity 100.0%; Pred. No. 0.00011; Mismatches 0; Indels 0; Gaps 0;
 Matches 18; Conservative 0;
 Qy 1 RLLRAVIMGAPGSGKGT 18
 Db 35 RLLRAVIMGAPGSGKGT 52
 RESULT 12
 AAB12441
 ID AAB12441 standard; Protein; 227 AA.
 AC AAB12441;
 XX
 DT 20-OCT-2000 (first entry)
 XX
 DE AK3 protein sequence.
 XX
 KW Human; mitochondrial GTP:AMP phosphotransferase; GTP3P; ribotide.
 XX
 OS Unidentified.
 XX
 PN CN1249340-A.
 XX
 PD 05-APR-2000.
 XX
 PR 28-SEP-1998; 98CN-0119439.

PR	28-SEP-1998;	98CN-0119439.	PN	WO200181555-A2.
XX			XX	
PA	(XINH-)	XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.	PD	01-NOV-2001.
XX			XX	
PI	Yu L, Zhao Y, Bi A;		PF	20-APR-2001; 2000US-199021P.
XX			PR	20-APR-2000; 2000US-200226P.
DR	WPT; 2000-400718-35.		PR	28-APR-2000; 2000US-202339P.
DR	N-PSDB; AAA60585.		PR	05-MAY-2000; 2000US-203505P.
PT	Preparation of human mitochondrial matrix GTP : AMP phosphotransferase, its encode sequence		PR	18-MAY-2000; 2000US-205564P.
XX	Sequence 227 AA;		PR	26-MAY-2000; 2000US-207739P.
PS	Example 2; Fig 2; 20pp; Chinese.		PR	01-JUN-2000; 2000US-208795P.
XX			XX	
CC	The present invention describes a new ribotide sequence of human gene, that is, the cDNA sequence of human mitochondrial matrix GTP:AMP phosphotransferase (GTP3P) and the encoded polypeptide. The present sequence represents the AK3 protein sequence which is used in comparison with human GTP3P in the present invention.		PA	(INCY-) INCYNE GENOMICS INC.
CC	CC		XX	Yue H, Gandhi AR, Tribouley CM, Kearney L, Griffin JA, Nguyen DB; PI Bandman O, Lu DAM, Ial P, Burhill JD, Marcus GA, Zingler KA, Recipon SK, Lu Y; Patterson C, Burhill JD, Marcus GA, Zingler KA, Recipon SK, Lu Y; PI Policky JL, Thornton M, Tang YI, Hafalla A, Elliott VS, Baughn MR; Walsh RR, Ramkumar J, Borowsky ML, Au-young J, Hillman JT; PI Gururajan R;
CC	XX		XX	XX
QY	Query Match 95.5%; Score 84; DB 21; Length 227; Best Local Similarity 94.4%; Pred. No. 0.0037; Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		DR	WPT; 2001-611740770.
Db	6 RLLRAVINGAPGSGKGTv 23		DR	N-PSDB; AADI8827.
PS			XX	
RESULT 13			XX	
AAB1178			CC	The present invention relates to human kinases (PKIN) and the nucleic acids encoding them. PKIN is used as vaccine and in gene therapy. PKIN is used in the prevention, diagnosis and treatment of diseases cancers, adenocarcinoma, sarcoma, immune disorder, Addison's disease, acquired immune deficiency syndrome (AIDS), anaemia, asthma, allergies, gout, microbial infections, cardiovascular disease and/or inflammation, masthenia gravis, atherosclerosis, cirrhosis, osteoporosis, mycardial infarction, cataract, growth and development disorder, seizure disorder, pulmonary embolism, Gaucher's disease, lipid disorder, lipid storage disease, Pick's disease, Tay-Sachs disease, renal disease and obesity.
ID	AAB1178 standard; Protein; 224 AA.		CC	PKIN may be used to treat disorders associated with decreased PKIN expression by rectifying mutations or deletions in a patient's genome that affect the activity of PKIN by expressing inactive proteins or to supplement the patients own production of PKIN. PKIN nucleic acids may be used to produce the PKIN polypeptide, by inserting the nucleic acids into a host cell and culturing the cell to express the protein. PKIN nucleic acid and its complementary sequences may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples and therefore which patients may be in need of restorative therapy. The present sequence is human PKIN-12 protein.
XX			CC	CC
AC	AAB1178;		CC	
XX			CC	
DE	18-DEC-2001 (first entry)		CC	
XX			CC	
DE	Human kinase (PKIN)-12 protein.		CC	
XX			CC	
KW	Human kinase; PKIN; gene therapy; adenocarcinoma; immune disorder; gout; cancer; allergy; sarcoma; leukaemia; acquired immune deficiency syndrome; AIDS; Addison's disease; microbial infection; inflammation; osteoporosis; atherosclerosis; cardiovascular disease; myocardial infarction; anaemia; masthenia gravis; cirrhosis; cataract; growth and development disorder; seizure disorder; pulmonary embolism; Gaucher's disease; lipid disorder; lipid storage disease; Pick's disease; Tay-Sachs disease; renal disease; obesity; restorative therapy; immunomodulatory; vaccine; cardiovascular; antimicrobial; cytostatic; antiinflammatory; asthma; OS Homo sapiens.		CC	
XX			CC	
FH	Key Location/Qualifiers		CC	
FT	Region 1..126 /note= "Adenylate kinase"		CC	
FT	Region 8..23 /note= "Shikimate kinase family"		CC	
FT	Region 9..25 /note= "Adenylate kinase"		CC	
FT	Region 10..190 /note= "Adenylate kinase"		CC	
FT	Region 33..76 /note= "Adenylate kinase"		CC	
FT	Region 80..94 /note= "Adenylate kinase"		CC	
FT	Region 85..96 /note= "Adenylate kinase motif"		CC	
FT	Region 107..124 /note= "Shikimate kinase family"		CC	
FT	Region 132..162 /note= "Adenylate kinase"		CC	
XX			CC	
RESULT 14			CC	
ABB62530	Query Match 87.5%; Score 77; DB 22; Length 224; Best Local Similarity 83.3%; Pred. No. 0.0035; Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;		ID	ABB62530 standard; Protein; 216 AA.
AC	QY 1 RLLRAVINGAPGSGKGTv 18		XX	ABB62530.
XX	Db 4 KLLRAVILGGPAPGSGKGTv 21		XX	
DE			XX	26-MAR-2002 (first entry)
DE	Drosophila melanogaster polypeptide SEQ ID NO 14382.		XX	

XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO00171042-A2.
XX
PD 27-SEP-2001.
XX
PT 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
N-PSDB; ABL06633.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 14382; 21pp + Sequence Listing; English.
XX
The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating the cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL0180-ABL16176, expressed DNA
CC sequences (ABL0180-ABL16175) and the encoded proteins
CC (ABL5737-ABL7207).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp://wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences).
XX
Sequence 216 AA:
SQ Query Match 84.1%; Score 74; DB 22; Length 216;
Best Local Similarity 72.2%; Pred. No. 0.0088; 4; Mismatches 13; Conservative 13;
Matches 13; Indels 0; Gaps 0;
OY 1 RLIRRAVIMGAPSGSGKGTV 18
Db 4 KIERRAVIGAPSGSGKGTI 21
Db 4 KIERRAVIGAPSGSGKGTI 21
RESULT 15
AAB53619
ID AAB53619 standard; Protein; 214 AA.
XX
AC AAB53619;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human colon cancer antigen protein sequence SEQ ID NO:1179.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytosolic; cardioactive; neuroprotective; vulnerary;
KW immunomodulatory; muscular; gynecological; gastrointestinal;
KW nephrotoxic; antiflектив; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder.
XX
OS Homo sapiens.
XX
PN WO200053351-A1.

PD 21-SEP-2000.
XX
PR 08-MAR-2000; 2000MO-US05883.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PT Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
XX
N-PSDB; AAC9876.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer -
XX
PS Claim 11; Page 171-172; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytosolic, cardioactive, muscular,
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC pulmonary, nephrotoxic, anti-infective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins
CC may also be used to prevent diseases such as neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, wounds, renal disorders, infectious
CC diseases and cardiovascular disorders. AAC98764 to AAC98772 and
CC AAB4007 represent sequences used in the exemplification of the present
CC invention.

SQ Sequence 214 AA;
SQ Query Match 79.5%; Score 70; DB 21; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.032; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 AVIMGAPSGSGKGTV 18
Db 1 AVIMGAPSGSGKGTV 14
Search completed: April 24, 2003, 10:19:29
Job time : 37 secs



GenCore version 5.1.4-p5_4578
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OM protein - protein search, using sw model
 Run on: April 24, 2003, 10:17:37 ; Search time 29 Seconds
 (without alignments)
 127.891 Million cell updates/sec

Title: US-10-006-190-1_COPY_6_23
 Perfect score: 88
 Sequence: RLLRAVIMGAPGSGKGTV 18
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5
 Searched: 671580 seqs, 206047115 residues
 Total number of hits satisfying chosen parameters: 671580
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SPREMBL_21:
 1: sp_archeap: *
 2: sp_bacteria: *
 3: sp_fungi: *
 4: sp_human: *
 5: sp_invertebrate: *
 6: sp_mammal: *
 7: sp_mhc: *
 8: sp_organelle: *
 9: sp_phage: *
 10: sp_plant: *
 11: sp_rabbit: *
 12: sp_virus: *
 13: sp_vertebrate: *
 14: sp_unclassified: *
 15: sp_rvirus: *
 16: sp_bacteriap: *
 17: sp_archeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	IB	Description
1	88	100.0	189	11	Q9DBW6		Q9dbw6 mus musculu
2	88	100.0	227	4	Q9NPB4		Q9npb4 homo sapien
3	88	100.0	227	6	Q95J94		Q95j94 oryctolagus
4	88	100.0	227	11	Q9DBM5		Q9dbm5 mus musculu
5	88	100.0	227	11	Q9DB57		Q9db57 mus musculu
6	88	100.0	227	11	Q9DB71		Q9db71 mus musculu
7	74	84.1	216	5	Q9VG6		Q9vg6 drosophila
8	65	73.9	231	3	Q93985		Q93985 neocallimmas
9	65	73.9	231	3	Q93987		Q93987 pirimorces
10	64	72.7	232	3	Q93986		Q93986 neocallimmas
11	62	70.5	55	2	Q9D16		Q9d16 bacteroides
12	60	68.2	194	2	Q9KWA2		Q9kwa2 agrobacteri
13	60	68.2	202	4	Q8TCY3		Q8tcy3 homo sapien
14	60	68.2	232	11	Q9CY37		Q9cy37 mus musculu
15	58	65.9	130	11	Q8RA46		Q8ra46 mus musculu
16	58	65.9	248	11	Q9ESCA4		Q9esc4 mus musculu

RESULT 1

ID	Q9DBW6	PRELIMINARY	PRT:	189 AA.
AC	Q9DBW6;			
DT	01-JUN-2001 (TREMBBLE, 17, Created)			
DT	01-JUN-2001 (TREMBBLE, 17, last sequence update)			
DE	10 day old male porcine CDNA, RIKEN full-length enriched library, clone:1810027K10, full insert sequence.			
OS	Mus musculus (Mouse); Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CC7BL/6J; TISSUE=PANCRAS;			
RX	MEDLINE=21085660; PubMed=12127851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto I., Saito T., Okasaki Y., Gotobori T., Bono H., Kasukawa T., Saito R., Kondo K., Matsuda H.A., Ashburner M., Batalov S., Cassavant T., Fleischmann W., Gaasterland T.R., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsu S., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blaize J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fleischer C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniwa M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaiji H., Kohtsukii S., Hayashizaki Y.;			
RA	"Functional annotation of a full-length mouse cDNA collection.;" Nature 409:685-690 (2001); "SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY. EMBL: AK007618; BAB25139; 1; -.			
DR				

ALIGNMENTS

DR HSSP; PR08760; 2AK3
 DR InterPro; IPR000850; Adenylylate_kin.
 DR InterPro; IPR000623; Shik_kinase.
 DR Pfam; PF00056; adenylylate kinase; 1.
 DR PRINTS; PR00054; ADENYLYLKNASE.
 DR PRINTS; PR01100; SHIKIMIKINASE.
 DR PRODOM; PD000557; Adenylylate_kin; 1.
 DR PROSITE; PS00113; ADENYLYLATE_KINASE; 1.
 DR KW kinase; Transferase.
 SQ SEQUENCE 189 AA; 21193 MW; 832ADB21804F5336 CRC64;

Query Match 100.0%; Score 88; DB 11; Length 189;
 Best Local Similarity 100.0%; Pred. No. 6.2e-05; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;

Db 6 RLLRAVIMAGPGSGKTV 23

RESULT 2

Q9NFB4 PRELIMINARY; PRT; 227 AA.

ID Q9NFB4; AC Q9NFB4; DT 01-OCT-2000 (TREMBrel. 15, Created)
 DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)

DE CDNA FLJ11089 fis, clone Place1005305 highly similar to GTP:AMP
 DE phosphotransferase mitochondrial (EC 2.7.4.10) (CDNA FLJ10691 fis,
 DE clone NTZRP300359, highly similar to GTP:AMP phosphotransferase
 DE mitochondrial) (CDNA FLJ14628 fis, clone NTZRP200329, highly similar
 DE to GTP:AMP phosphotransferase mitochondrial) (Hypothetical 25.6 kDa
 DE protein).

OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
 OC NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Aotsuka S., Yoshihawa Y.,
 RA Matsumura H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
 RA Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
 RT "NEDO human cDNA sequencing project.";
 RL [2] Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirooka S., Ishii S., Kawai Y.,
 RA Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
 RA Masuho Y., Kanehori K.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiroiwa T., Sudo H., Saito K.,
 RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanebe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RL "NEDO human cDNA sequencing project.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LYMPH;
 RA Straubberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.

Query Match 100.0%; Score 88; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;

Db 6 RLLRAVIMAGPGSGKTV 23

RESULT 3

Q95U94 PRELIMINARY; PRT; 227 AA.

ID Q95U94; AC Q95U94; DT 01-DEC-2001 (TREMBrel. 19, Created)
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)

DE Adenylylate kinase 3.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TAXID=9906;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=RENAL PROXIMAL TUBULE;
 RA MEDLINE=21240335; PUBMED=1142145;
 RA Brochiero E., Coady M.J., Klein H., Laprade R., Lapointe J.Y.,
 RA "Activation of an ATP-dependent K(+) conductance in Xenopus oocytes by
 RA expression of adenylylate kinase cloned from renal proximal tubules.";
 RA RL Biochim. Biophys. Acta 1510:29-42(2001).
 RA CC -1 SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
 RA DR EMBL; AF017508; AAU07503; 1. -
 RA DR InterPro; IPR000850; Adenylylate_kin.
 RA DR Pfam; PF00406; adenylylate_kin.
 RA DR PRODOM; PD000557; Adenylylate_kin; 1.
 RA DR PROSITE; PS00113; ADENYLYLATE_KINASE; UNKNOWN_1.
 RA SQ SEQUENCE 227 AA; 25610 MW; ECD1DDFA89228A4E CRC64;

Query Match 100.0%; Score 88; DB 6; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;

Db 6 RLLRAVIMAGPGSGKTV 23

RESULT 4

Q9DBM5 PRELIMINARY; PRT; 227 AA.

ID Q9DBM5; AC Q9DBM5; DT 01-JUN-2001 (TREMBrel. 17, Created)
 DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBrel. 17, Last annotation update)
 DT 01-MAR-2002 (TREMBrel. 20, Last annotation update)

DE Adenylylate kinase 3 alpha like.
 GN AKL3L.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N_A.
 RP STRAIN=C57BL/6J; TISSUE=LIVER;
 RC MEDLINE=2108560; PubMed=11217851;
 RX RA Kawai J., Shinagawa A., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai H., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fukuda M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittraker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
 DR EMBL: AK005194; BAB23876.1. -.
 DR HSSP: P08766; 2AK3.
 DR PRINTS: PR0100; SHKIMTKNASE.
 DR PRODOM: PD000657; Adenylylate_kin; 1.
 DR PROSITE: PS00113; ADENYLYLATE_KINASE; 1.
 DR KINASE; Transferase.
 SQ SEQUENCE 227 AA; 25427 MW; 680DF1E991DE5AC CRC64;
 Query Match 100.0%; Score 88; DB 11; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR QY 1 RLLRAVIMGAPGSGKTV 18
 1 ||||| ||||| ||||| |||||
 Db 6 RLLRAVIMGAPGSGKTV 23
 RESULT 5
 Q9DB57 PRELIMINARY; PRT; 227 AA.
 ID Q9DB57; PRELIMINARY; PRT; 227 AA.
 AC 09DB57;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE Adenylate kinase 3 alpha like.
 GN AK13L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N_A.
 RP STRAIN=C57BL/6J; TISSUE=STOMACH;
 RC MEDLINE=2108560; PubMed=11217051;
 RX RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sasaki H., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fukuda M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittraker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
 DR EMBL: AK005194; BAB23876.1. -.
 DR HSSP: P08766; 2AK3.
 DR PRINTS: PR00094; ADENYLYLTKNASE.
 DR PRINTS: PR01100; SHKIMTKNASE.
 DR PRODOM: PD000657; Adenylylate_kin; 1.
 DR PROSITE: PS00113; ADENYLYLATE_KINASE; 1.
 DR KINASE; Transferase.
 SQ SEQUENCE 227 AA; 25427 MW; 660B7FBA971DE5AC CRC64;
 Query Match 100.0%; Score 88; DB 11; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DR QY 1 RLLRAVIMGAPGSGKTV 18
 1 ||||| ||||| ||||| |||||
 Db 6 RLLRAVIMGAPGSGKTV 23
 RESULT 6
 Q9D7Z1 PRELIMINARY; PRT; 227 AA.
 ID Q9D7Z1; PRELIMINARY; PRT; 227 AA.
 AC 09D7Z1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DE Adenylate kinase 3 alpha like.
 GN AK13L.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N_A.
 RP STRAIN=C57BL/6J; TISSUE=STOMACH;
 RC MEDLINE=2108560; PubMed=11217051;
 RX RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sasaki H., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fukuda M., Garibaldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittraker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
 DR EMBL: AK005194; BAB23876.1. -.
 DR HSSP: P08766; 2AK3.
 DR PRINTS: PR00094; ADENYLYLTKNASE.
 DR PRINTS: PR01100; SHKIMTKNASE.
 DR PRODOM: PD000657; Adenylylate_kin; 1.
 DR PROSITE: PS00113; ADENYLYLATE_KINASE; 1.
 DR KINASE; Transferase.
 SQ SEQUENCE 227 AA; 25427 MW; 660B7FBA971DE5AC CRC64;

RP SEQUENCE FROM N.A.
 RC TISSUE->COLON;
 RA STRAUSBERG R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 SEQUENCE FROM N.A.
 RA STRAUSBERG R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 SEQUENCE FROM N.A.
 RA STRAUSBERG R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 -1- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
 DR EMBL: AAK08681; BAB25829.1; -
 EMBL: B016432; AAH16432.1; -
 EMBL: B0219174; AAH19174.1; -
 EMBL: B024871; AAH24871.1; -
 HSSP: P08760; ZAK3.
 MGD: MGI:1860835; Ak131.
 InterPro: IPR000850; adenylylate_kin.
 InterPro: IPR000633; Shik_kinase.
 DR Pfam: PF00406; adenylylatekinase; 1.
 DR PRINTS: PR0094; ADENYLYTKINASE.
 DR PRINTS: PR0100; SHIKMTKINASE.
 DR PRODOM: PD00667; Adenylylate_kin; 1.
 DR PROSITE: PS00113; ADENYLYLATE_KINASE; 1.
 DR KW Kinase; Transferase.
 SEQUENCE 227 AA: 25426 MW: 6601DF10971DE5AC CRC64;
 Query Match 100.0%: Score 88; DB 11; Length 227;
 Best Local Similarity 100.0%; Pred. No. 7.5e-05; Mismatches 0;
 Matches 18; Conservative 0; Indels 0; Gaps 0;
 DR QY 1 RLLRAVINGAPGSGKGTV 18
 Db 6 RLLRAVINGAPGSGKGTV 23
 RESULT 7
 Q91GU6 PRELIMINARY; PRT: 216 AA.
 AC 091GU6 DR
 DT 01-MAY-2000 (TREMUREL, 13, Created)
 DT 01-MAY-2000 (TREMUREL, 13, Last sequence update)
 DT 01-MAR-2002 (TREMUREL, 20, Last annotation update)
 DE CG6612 protein (Adenylylate kinase isozyme 3).
 DE ADK3 OR CG6612.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriodea; Drosophilidae; Drosophila.
 OX NCBI_TAXID=727;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE-20106006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Changue M., Pfaffler B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heitz G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernhart B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burts K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Danile C., Devonport L.B., Davies P.,
 RA de Pablo B., Delchev A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hoskin D., Houston K.A., Howland T.J., Wei M.-H., Inegwam C.,
 RA Kimmel B.E., Kausch F., Karpen G.H., Ke Z., Kennison J.A., Ketchum R.A.,
 RA Lasko P., Lei Y., Levin斯基 A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshin N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacileb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purvi V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Slaten-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*.",
 RA Science 287:2185-2195 (2000).
 RN [2]
 SEQUENCE FROM N.A.
 RA Nona T.;
 RT DR
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
 DR EMBL: AR003669; AA#P54578.1; -
 DR EMBL: AR050622; BAB4152.1; -
 DR HSSP: P08760; ZAK3.
 DR InterPro: IPR000850; adenylylatekinase; 1.
 DR Pfam: PF00406; adenylylatekinase.
 DR PRINTS: PR00094; ADENYLYTKINASE.
 DR PRODOM: PD00667; Adenylylate_kin; 1.
 DR PROSITE: PS00113; ADENYLYLATE_KINASE; 1.
 DR KW Kinase; Transferase.
 SQ RESULT 8
 Q91GU6 PRELIMINARY; PRT: 216 AA.
 AC 091GU6 DR
 DT 01-MAY-1999 (TREMUREL, 10, Created)
 DT 01-MAY-1999 (TREMUREL, 10, Last sequence update)
 DT 01-MAR-2002 (TREMUREL, 20, Last annotation update)
 DE Adenylylate kinase (EC 2.7.4.3) (Fragment).
 DR HDGKL2.1.
 OS Neocallimastix frontalis (Rumen fungus).
 OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
 OC Neocallimastigomycetidae; Neocallimastix.
 OX NCBI_TAXID=4757;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN-12;
 RA Voncken F., Boxma B., Verhaegen E., van Wesel R., van der Drift C.,
 RA Veenhuis M., Hackstein J., Vogels G.;
 RA "Evidence for a chimeric origin of chytrid hydrogenosomes.",
 RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.
 DR EMBL: AU224558; CAA12055.1; -
 DR HSSP: P07170; IAKY.
 DR InterPro: IPR000850; Adenylylate_kin.
 DR Pfam: PF00406; adenylylatekinase; 1.

DR PRINTS; PRO0094; ADENYLTKNASE.
 DR Problem; PD00057; Adenylylate_kin; 1.
 PROSITE; PS00113; ADENYLATE_KINASE; 1.
 KW Kinase; Transferase.
 FT NON_TER 231 AA; 25353 MW; 844B51EB554676A2 CRC64;
 SQ SEQUENCE 231 AA; 25353 MW; 844B51EB554676A2 CRC64;
 Query Match 73.9%; Score 65; DB 3; Length 231;
 Best Local Similarity 86.7%; Pred. No. 0.14;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 LRAVIMGARGSGKGT 17
 FT ||||| ||||| 232 MW; 1B74EFD7C97891F2 CRC64;
 DB 10 LRMVIMGPPGSGKGT 24

RESULT 9
 ID 093987 PRELIMINARY; PRT; 231 AA.
 AC 093987;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DR Adenylylate kinase (EC 2.7.4.3) (Fragment).
 GN HDGAKKE2.
 OS Piromyces sp. E2.
 OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
 OC Neocallimasticaceae; Piromyces.
 OX NCBI_TAXID=73668;
 RN [1] SEQUENCE FROM N.A.
 RA Voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C.,
 RA Veenhuis M., Hackstein J., Vogels G.;
 RA "Evidence for a chimeric origin of chytrid hydrogenosomes.;"
 RA Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR PROTEIN; PS00113; ADENYLATE_KINASE.
 DR PRINTS; PRO0094; ADENYLTKNASE.
 DR Problem; PD00057; Adenylylate_kin; 1.
 DR HSSP; P01170; IAKY.
 DR InterPro; IPR000850; Adenylylate_kin.
 DR Pfam; PF0046; adenylylatekinase; 1.
 DR PRINTS; PRO0094; ADENYLTKNASE.
 DR Problem; PD00057; Adenylylate_kin; 1.
 DR PROTEIN; PS00113; ADENYLATE_KINASE; 1.
 DR Kinase; Transferase.
 KW Kinase; Transferase.
 FT NON_TER 231 AA; 25441 MW; 1B74EFD7C97891F2 CRC64;
 SQ SEQUENCE 232 AA; 25441 MW; 1B74EFD7C97891F2 CRC64;

Query Match 72.7%; Score 64; DB 3; Length 232;
 Best Local Similarity 80.0%; Pred. No. 0.19;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 LRAVIMGAGSGKGT 17
 DB 10 LRMVIMGPPGSGKGT 24

RESULT 11
 ID 09XD16 PRELIMINARY; PRT; 55 AA.
 AC 09XD16;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DR Adenylylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase)
 RN [1] (Fragment).
 OS Bacteroides fragilis.
 OC Bacteria; CFB Group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
 OC Bacteroides.
 OX NCBI_TAXID=817;
 RN [1] SEQUENCE FROM N.A.
 RA Comstock L.E., Coyne M.J., Tzianabos A.O., Pantosti A.,
 RA Onderdonk A.B., Kasper D.L.;
 RT "Analysis of a capsular polysaccharide biosynthesis locus of
 RT Bacteroides fragilis.;"
 RL Infect. Immun. 67:3525-3532(1999).
 CC -1 FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR
 CC MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
 CC -1 CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
 CC -1 SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1 SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 DR EMBL; AF048749; AF040729.1; -.
 DR HSSP; P2142; I2IN.
 DR InterPro; IPR000850; Adenylylate_kin.
 DR Pfam; PF0046; adenylylatekinase; 1.
 DR PRINTS; PRO0094; ADENYLTKNASE.
 DR Problem; PD00057; Adenylylate_kin; 1.
 DR KW ATP-binding; Kinase; Transferase.
 FT NON_TER 55 AA; 5849 MW; 027DC433E12908A CRC64;
 SQ SEQUENCE 55 AA; 5849 MW; 027DC433E12908A CRC64;

Query Match 70.5%; Score 62; DB 2; Length 55;
 Best Local Similarity 75.0%; Pred. No. 0.082;
 Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 LLRAVIMGAGSGKGT 17
 DB 1 MLNIVIFGAGSGKGT 16

RESULT 12
 RA voncken F., Boxma B., Verhagen E., van Wesel R., van der Drift C.,

Q9KWA2 PRELIMINARY; PRT; 194 AA.
 Q9KWA2; ID :| :|||·|||||
 AC 1 MRLILMGPAGPSGKGT 15
 DT 01-OCT-2000 (TREMBREL. 15, Created)
 DT 01-OCT-2000 (TREMBREL. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBREL. 20, Last annotation update)
 DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
 DR ADK OR RIOPR82.
 OS Agrobacterium rhizogenes.
 OC Plasmid PR11724.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Rhizobium.
 OX NCBI_TAXID=359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01124; PLASMID=PR11724;
 RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;
 RT "Analysis of unique variable region of a plant root inducing Plasmid, PR11724, by the construction of its physical map and library.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01124; PLASMID=PR11724;
 RA Moriguchi K., Nishida T., Maeda Y., Tanaka N., Yoshida K.;
 RT "Genome structure of R1 Plasmid (1); Construction of linking library and physical map of pl11724 from Japanese Agrobacterium.";
 RL Nucleic Acids Symp. Ser. 39:189-190(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01124; PLASMID=PR11724;
 RA Moriguchi K., Maeda Y., Satou M., Satuti N., Kataoka M., Tanaka N., Yoshida K.;
 RT "The complete nucleotide sequence of a R1 (root inducing) plasmid indicates its chemical structure between Ti and Sym plasmids.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01124; PLASMID=PR11724;
 RA Moriguchi K., Maeda Y., Satou M., Kataoka M., Tanaka N., Yoshida K.;
 RT "Analysis of unique variable region of a plant root inducing Plasmid, PR11724, by the construction of its physical map and library.";
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF03-01124; PLASMID=PR11724;
 RA Maeda Y., Moriguchi K., Kataoka M., Satou M., Tanaka N., Yoshida K.;
 RT "Genome structure of R1 plasmid (1); Sequencing analysis of T-DNA and its flanking regions of PR11724 in Japanese Agrobacterium rhizogenes";
 RL Nucleic Acids Symp. Ser. 42:67-68(1999).
 RC MAINTENANCE AND CELL GROWTH IS ESSENTIAL FOR FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: AMP + AMP = ADP + ADP.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
 EMBL: AB039332; BAA97793; 1. --.
 ENBM: AP002086; BAB16201; 1. --.
 DR HSP; P0170; LAKY.
 DR InterPro; IPR00050; Adenylate_kin.
 DR Pfam; PF00406; adenylatekinase; 1.
 DR PRINTS; PR0094; ADENYLKINASE.
 DR PRODOM; PD000657; Adenylate_kin; 1.
 DR PROSITE; PS00113; ADENYLATE_KINASE; 1.
 DR ATP-binding_Kinase; Plasmid_Transferase.
 SQ SEQUENCE; 194 AA; 20468 MW; 533450AEF084F59 CRC64;
 Query Match 68.2%; Score 60; DB 2; Length 194;
 Best Local Similarity 66.7%; Pred. No. 0.58;
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 LRAVIMGPGSGKGT 17
 ID Q9CY37
 AC Q9CY37;
 DT 01-JUN-2002 (TREMBREL. 21, Created)
 DT 01-JUN-2002 (TREMBREL. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBREL. 21, Last annotation update)
 DE Adenylate kinase 2 variant AK2C.
 RN AK2.
 RP SEQUENCE FROM N.A.
 RA Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homino. NCBI_TAXID=606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Guo J.;
 RL "Novel Isoforms of Human Adenylate Kinase 2.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AY080599; AAL87027.1; --.
 DR KW Kinase.
 SQ SEQUENCE 202 AA; 22265 MW; AE7593A8ADBD00CF CRC64;
 Query Match 68.2%; Score 60; DB 4; Length 202;
 Best Local Similarity 66.7%; Pred. No. 0.5; Mismatches 4; Mismatches 1; Indels 0; Gaps 0;
 Matches 10; Conservative 4; DE Adenylate kinase 2.
 QY 3 LRAVIMGPGSGKGT 17
 ID Q9CY37
 AC Q9CY37;
 DT 01-JUN-2001 (TREMBREL. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBREL. 20, Last annotation update)
 DE Adenylate kinase 2.
 RN AX2.
 RP SEQUENCE FROM N.A.
 RC STRAIN=NC57BL/6J; Published=11217051;
 RA Kawai J., Shinzawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Iizawa K., Iwasa M., Nishi K., Kiyosawa H., Kondo S., Yamamoto T., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann R., Gaasterland T., Gissi C., Hume D.A., Kameya T., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Stabili F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibaldi M., Gustinovich S., Hill D., Hofmann M., Hume D.A., Kameya T., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Rodriguez T., Sakamoto N., Washio T., RA Suzuki H., Sato K., Schoenbach C., Suya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Brownshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).

[2]

SEQUENCE FROM N.A.

RP

RA ;

Strausberg R.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

CC -!- SIMILARITY: BELONGS TO THE ADENYLYLATE KINASE FAMILY.

DR EMBL: AK010951; BAR27286_1; -.

DR EMBL: BC008610; AAH08610_1; -.

DR HSSP; P08166; IAK2.

DR MGI: 87978; Ak2.

DR InterPro; IPR000850; Adenylate_kinase_1.

DR Pfam; PF00406; adenylylatekinase_1.

DR PRINTS; PR0094; ADENYLTKINASE.

DR PRODOM; PD00657; Adenylate_kin_1.

DR PROSITE; PS00113; ADENYLYLATE_KINASE_1.

KW Kinase; Transferase.

SQ SEQUENCE 232 AA; 25605 MW; EDD60400562323CF CRC64;

Query Match 68.2%; Score 50; DB 11; Length 232;

Best Local Similarity 66.7%; Pred. No. 0.69;

Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 LRAVIMGARGSGKGT 17

Db 16 ITRAVLGLPFGAKGT 30

RESULT 15

Q8R4A6 PRELIMINARY; PRT; 130 AA.

ID Q8R4A6;

AC Q8R4A6;

DT 01-JUN-2002 (TREMBiReL 21, Created)

DT 01-JUN-2002 (TREMBiReL 21, Last sequence update)

DT 01-JUN-2002 (TREMBiReL 21, Last annotation update)

DE ERA-like protein 1 (fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;

RA Ji Z., Chen S., Liu J., Zhao Z., Chai Y., Liu X., Chen N.;

RT "Mouse chromosome 11.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

EMBL: AA48635; AAM08321_1; -

FT NON-TER 1

FT 130

SQ SEQUENCE 130 AA; 13005 MW; 3BB0749DAE63C5BB CRC64;

Query Match 65.9%; Score 58; DB 11; Length 130;

Best Local Similarity 55.6%; Pred. No. 0.73;

Matches. 10; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 RLRAVIMGARGSGKGT 18

Db 16 ITRAVLGLPFGAKGT 30

78 RVLRVVLGAPNACKSTL 95

Search completed: April 24, 2003, 10:18:17

Job time : 32 secs

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